Law Offices
FOLEY & LARDNER
Suite 500
3000 K Street, N.W.
Washington, DC 20007-5109
(202) 672-5300

TO: Assistant Commissioner for Patents
Box Patent Applications
Washington D.C. 20231

Attorney Docket No.16761/153

UTILITY PATENT APPLICATION TRANSMITTAL
(new nonprovisional applications under 37 CFR 1.53(b))

Transmitted herewith for filing is the patent application of:

INVENTOR(S): Roy A. BLACK, Raymond James PAXTON, Wolfram BODE, Klaus MASKOS, Carlos FERNANDEZ-CATALAN, James Ming CHEN, and Jeremy Ian LEVIN

TITLE: CRYSTALLINE TNF-α-CONVERTING ENZYME AND USES THEREOF

In connection with this application, the following are enclosed:

APPLICATION ELEMENTS:

XX Specification - 91 TOTAL PAGES

XX Drawings - Total Sheets 7

__ Declaration and Power of Attorney - Total Sheets __

- _ Newly executed (original or copy)
- _ Copy from a prior application (37 CFR 1.63(d)) (relates to continuation/divisional boxes completed) - NOTE: Box below
- _ DELETION OF INVENTOR(S) - Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).

__ Incorporation By Reference (useable if copy of prior application Declaration being submitted)

The entire disclosure of the prior application, from which a COPY of the oath or declaration is supplied as noted above, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

__ Microfiche Computer Program (Appendix)

__ Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)

- __ Computer Readable Copy
- __ Paper Copy (identical to computer copy)
- __ Statement verifying identify of above copies

ACCOMPANYING APPLICATION PARTS

__ Assignment Papers (cover sheet & document(s))
__ 37 CFR 3.73(b) Statement (when there is an assignee)
__ English Translation Document (if applicable)
__ Information Disclosure Statement(IDS) with PTO-1449. __ Copies of IDS Citations
__ Preliminary Amendment
XX Return Receipt Postcard (MPEP 503)
__ Small Entity Statement(s)
  __ Statement file in prior application, status still proper and desired.
__ Certified Copy of Priority Document(s) with Claim of Priority (if foreign priority is claimed).
__ OTHER:

CORRESPONDENCE ADDRESS:

Foley & Lardner Address noted above.
Telephone: (202) 672-5300
Fax Number: (202) 672-5399

FEE CALCULATIONS: (Small entity fees indicated in parentheses.)

(1) For	(2) Number Filed	(3) Number Extra	(4) Rate	(5) Basic Fee $760 ($380)
Total Claims	62 - 20 =	42	x $18 (x $9)	756.00
Independent Claims	9 - 3 =	6	x $78 (x $39)	468.00
Multiple Dependent Claims			$260 ($130)	
Assignment Recording Fee per property			$40	
Surcharge Under 37 C.F.R. 1.16(e)			$130 ($65)	
			TOTAL FEE:	$1,984.00

METHOD OF PAYMENT:
A check in the amount of the above TOTAL FEE is attached. If payment by check is NOT enclosed, it is requested that the Patent and Trademark Office advise the undersigned of the period of time within which to file the TOTAL FEE. If payment enclosed, this amount is believed to be correct; however, the Commissioner is hereby authorized to charge any deficiency or credit any overpayment to Deposit Account No. 19-0741.

Respectfully submitted,

John P. Isacson
Reg. No. 33,715

Date: February 4, 1999
Docket No.: 16761/153

Attorney Docket No.: 16761/153

Inventors: Roy A. Black
Raymond James Paxton
Wolfram Bode
Klaus Maskos
Carlos Fernandez-Catalan
James Ming Chen
Jeremy Ian Levin

TITLE OF THE INVENTION

Crystalline TNF-α-Converting Enzyme and Uses Thereof

INFORMATION ON RELATED APPLICATIONS

This application claims the priority benefit of U.S. provisional patent application serial No. 60/073,709, filed February 4, 1998, U.S. patent application serial No. 09/050,083, filed March 30, 1998 (which will be converted to a US provisional application pursuant to a petition filed on January 27, 1999), and US provisional patent application titled "Crystalline TNF-α-Converting Enzyme and Uses Thereof," filed January 27, 1999.

BACKGROUND OF THE INVENTION

The cytokine tumor necrosis factor-α (TNFα) plays a role in the induction of inflammatory reactions and is known to be cytotoxic towards tumor cells. TNFα, however, also may cause severe damage to the human body when produced in excess by eventually leading to multiple organ failure and death. See Bemelmans *et al.*, "Tumor Necrosis Factor: Function, Release and Clearance," *Crit. Rev. Immun.* 16: 1-11 (1996).

Tumor necrosis factor-α is produced by activated cells, such as mononuclear phagocytes, T-Cells, B-Cells, mast cells and NK cells. TNFα exists in two forms: a type II membrane protein having a relative molecular mass of 26 kD and a soluble 17 kD form generated from the membrane form by proteolytic cleavage. The

TNFα membrane protein is synthesized as a 223 amino acid membrane-anchored precursor. The soluble TNFα is released from the membrane-bound precursor by a membrane-anchored proteinase. This proteinase was recently identified as a multidomain metalloproteinase called TNFα-converting enzyme (TACE). See, Black *et al.*, "A metalloproteinase disintigrin that releases tumor-necrosis factor-α from cells," Nature 385: 729-733 (1997), Moss *et al.*, "Cloning of a disintigrin metalloproteinase that processes precursor tumor-necrosis factor-α," Nature 385: 733-736 (1997). TACE has recently been identified as a zinc endopeptidase consisting of an extracellular region comprising an N-terminal signal peptide, a pro-domain, a 263 residue catalytic domain (TCD) that is preceded by a furin cleavage site (residues 211-214), a disintegrin domain, an EGF-like domain, and a crambin-like domain, an apparent transmembrane helix and the intracellular C-terminal tail. Tumor necrosis factor-α converting enzyme (TACE), including a polynucleotide sequence, is described in detail in the published PCT application No. WO 96/41624, herein incorporated in the entirety by reference.

As noted above, the over-production or unregulated production of TNFα presents serious physiological dangers. It has been implicated in various deleterious physiological diseases such as rheumatoid arthritis, cachexia and endotoxic shock. It also may eventually lead to organ failure and death. Thus, a way to control or block release of TNFα into the circulation is needed. Because of TACE's role in the conversion of TNFα, inhibition, modulation, or regulation of TACE would affect the release of TNFα into circulation. Inhibitors of metalloproteinases and structure based design thereof are described in Zask *et al.*, "Inhibition of Matrix Metalloproteinases: Structure Based Design" *Current Pharmaceutical Design*, 2:624-661 (1996). Thus, compounds that associate with TACE, such as inhibitors, receptors or modulators will be useful to protect patients from adverse effects associated with the over-production or unregulated production of tumor necrosis factor-α.

SUMMARY OF THE INVENTION

According to one aspect of the invention, there is provided a composition comprising a polypeptide in crystalline form, wherein the polypeptide is a TNF-α-converting enzyme polypeptide. In one embodiment, the TNF-α-converting enzyme polypeptide comprises the TNF-α-converting enzyme catalytic domain. In another embodiment, the TNF-α-converting enzyme polypeptide is the expression product of a polynucleotide encoding the pro and catalytic domains of TNF-α-converting enzyme. In a further embodiment, the TNF-α-converting enzyme polypeptide is the expression product of a polynucleotide encoding the amino acid residues 1-477 of TNF-α-converting enzyme. In yet another embodiment, the polynucleotide is substituted such that amino acid residue Ser266 is changed to Ala and amino acid residue Asn542 is changed to Gln, and wherein a second polynucleotide encoding the sequence Gly-Ser-$(His)_6$ is fused to the C-terminus.

According to another aspect of the invention, the compositions above further comprising a binding partner suitable for co-crystallization with the TNF-α-converting enzyme polypeptide. In one embodiment, the binding partner is a hydroxamate-based binding partner. In another embodiment, the binding partner is N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine,2-(amino)ethyl amide.

According to further embodiments, the compositions above have a crystal structure diffracting to 2.0 Å, are monoclinic, have a unit cell comprising four crystallographically independent TNF-α-converting enzyme catalytic domain (TCD) molecules, have the TCD molecules are in an asymmetric unit, and/or have monoclinic space group $P2_1$ and the cell has the constants a=61.38 A, b=126.27 A, c=81.27 A, and β=107.41°.

In still another embodiment of the invention, the polypeptides above are characterized by the structure coordinates according to Table 1, or a substantial part thereof.

According to a further aspect of the invention, there is provided a method for crystallizing a TNF-α-converting enzyme polypeptide, comprising (A) mixing a solution comprising a TACE polypeptide and a binding partner with a crystallization buffer; and (B) crystallizing the mixture of step (A) by drop vapor diffusion to form a crystalline precipitate. In one embodiment, the method further comprises (C) transferring seeds from the crystalline precipitate formed by the drop vapor diffusion and a crystallization promotor into a mixture of a concentrated solution comprising a TACE polypeptide and binding partner substrate, and a crystallization buffer; and (D) crystallizing the mixture of step (C) by drop vapor diffusion to form a crystal. In another embodiment, the crystallization buffer is 0.1M Na Citrate pH 5.4, 20%w/v PEG 4000, and 20% v/v Isopropanol. In still another embodiment, the binding partner is N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine, 2-(amino)ethyl amide. In yet another embodiment, crystallization is at a temperature ranging from 4 to 20 degrees Celsius. In another embodiment, the solution comprising the TACE polypeptide and the inhibitor is at a concentration of about 5 mg/mL to about 12 mg/mL in a buffer. In a further embodiment, the solution comprising a TACE polypeptide and the binding partner is mixed with the crystallization buffer in a 1:1 ratio.

According to still another aspect of the invention, there is provided a tumor necrosis factor-α (TNF-α)-converting enzyme crystal made by co-crystallizing a TNF-α-converting enzyme polypeptide with a co-crystallization substrate.

According to yet another aspect of the invention, there is provided a computer-readable medium having recorded thereon x-ray crystallographic coordinate data for the catalytic domain of TNF-α converting enzyme, or a portion

thereof. In one embodiment, the computer-readable medium has recorded thereon the x-ray crystallographic coordinate data set forth in Table 1, or a portion thereof. In another embodiment, the medium is selected from the group consisting of a floppy disc, a hard disc, computer tape, RAM, ROM, CD, DVD, a magnetic disk, and an optical disk. In still another embodiment, the computer-readable medium has recorded thereon machine-readable data, wherein the computer-readable medium, when used in conjunction with a machine programmed with instructions for using the data, is capable of generating image signals for depicting a graphical, three-dimensional representation of a TNF-α converting enzyme polypeptide, or portion thereof.

According to a further aspect of the invention, there is provided a system for studying a TNF-α converting enzyme polypeptide, said system comprising (a) a memory capable of storing information representing at least a portion of a TNF-α converting enzyme polypeptide, wherein said memory comprises at least one first-type storage region, including a set of spatial coordinates specifying a location in a three dimensional space, and at least one second-type storage region comprising information representing a characteristic of one of a plurality of amino acids, said second-type storage regions being logically associated with said first-type storage regions in said memory to represent a geometric arrangement of at least one characteristic of said at least a portion of said TNF-α converting enzyme peptide in said three dimensional space; (b) a processor coupled to said memory to access said first-type storage regions and said second-type storage regions, wherein the processor generates image signals for depicting a visual image representing three dimensional image of said at least one characteristic of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space based on data from said memory; and (c) a display coupled to said processor to receive said image signals, wherein the display depicts a visual three dimensional image of said at least one characteristic of said at least a portion of said TNF-α converting enzyme

polypeptide in said three dimensional space based on said image signals. In one embodiment of the invention, the image signals include signals for depicting a visual three dimensional image of a ribbon structure of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space. In another embodiment of the invention, the image signals include signals for depicting a visual image of a solid model representation of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space. In still another embodiment of the invention, the image signals include signals for depicting a visual three dimensional image of electrostatic surface potential of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space. In yet another embodiment of the invention, the image signals include signals for depicting a visual three dimensional stereo image of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space. In a further embodiment of the invention, the system further comprises a storage device capable of storing data representing a geometric arrangement of a characteristic of a composition other than said TNF-α converting enzyme polypeptide; and an operator interface for receiving instructions from a operator; and wherein said processor is coupled to said storage device and to said operator interface and generates additional image signals for depicting said geometric arrangement of said characteristic of said composition relative to said visual three dimensional image of said at least one characteristic of said at least a portion of said TNF-α converting enzyme polypeptide on said display based on instructions from the operator interface. In one embodiment, the storage device is part of said memory. In another embodiment, the system comprises a plurality of first-type and second-type storage regions.

According to another aspect of the invention, there is provided a video memory capable of storing information for generating a visual display of at least a portion of a TNF-α converting enzyme polypeptide, said video memory comprising

(a) at least one first-type storage region, each of said first-type storage regions including a set of spatial coordinates specifying a location in a three dimensional space; and (b) at least one second-type storage region, each of said second-type storage regions containing information for visually depicting a characteristic of one of a plurality of amino acids; wherein said second-type storage regions are logically associated with said first-type storage regions in said video memory to represent a geometric arrangement of at least one characteristic of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space. In one embodiment, the second-type storage regions are logically associated with said first-type storage regions in said video memory to represent a geometric arrangement of at least one characteristic of a catalytic domain portion of said TNF-α converting enzyme polypeptide in said three dimensional space. In another embodiment, the first-type storage regions and said second-type storage regions are regions of a semiconductor memory. In yet another embodiment, the first-type storage regions and said second-type storage regions are regions of an optical disk. In still another embodiment, the first-type storage regions and said second-type storage regions are regions of a magnetic memory. In a further embodiment, the video memory comprises a plurality of first-type and second-type storage regions.

In a still further aspect of the invention, there is provided a method of identifying a compound that associates with TNF-α-converting enzyme, comprising (A) designing an associating compound for said polypeptide that forms a bond with the TNF-α-converting enzyme catalytic domain based on x-ray diffraction coordinates of a TNF-α-converting enzyme polypeptide crystal; (B) synthesizing said compound; and (C) determining the associate capability of said compound with said TNF-α-converting enzyme. In one embodiment, the associating compound is an inhibitor, mediator, or other compound that regulates TNF-α-converting enzyme activity. In another embodiment, the associating compound is a competitive inhibitor, un-competitive inhibitor, or non-competitive inhibitor. In still another

embodiment, the coordinates are the coordinates of Table 1, or a substantial part thereof. In a further embodiment, the TNF-α-converting enzyme polypeptide crystal comprises the TNF-α-converting enzyme catalytic domain. In still another embodiment, the TNF-α-converting enzyme polypeptide is the expression product of a polynucleotide encoding the pro and catalytic domains of TNF-α-converting enzyme. In yet another embodiment, the TNF-α-converting enzyme polypeptide is the expression product of a polynucleotide encoding the amino acid residues 1-477 of TNF-α-converting enzyme. In another embodiment, the polynucleotide is substituted such that amino acid residue Ser266 is changed to Ala and amino acid residue Asn542 is changed to Gln, and wherein a second polynucleotide encoding the sequence Gly-Ser-$(His)_6$ is fused to the C-terminus. In a further embodiment, the TNF-α-converting enzyme polypeptide crystal is co-crystallized with a binding partner. In still another embodiment, the binding partner is a hydroxamate-based binding partner or N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine,2-(amino)ethyl amide. In yet other embodiments, the TNF-α-converting enzyme polypeptide crystal has a crystal structure diffracting to 2.0 Å, is monoclinic, has a unit cell comprising four crystallographically independent TNF-α-converting enzyme catalytic domain (TCD) molecules, has the TCD molecules are in an asymmetric unit, and/or is of monoclinic space group $P2_1$ and the cell has the constants a=61.38 Å, b=126.27 Å, c=81.27 Å, and β=107.41°. In still another embodiment, the invention the the associating compound is designed to associate with the S1' region of TNF-α-converting enzyme. In yet another embodiment, the associating compound is designed to associate with the S1'S3' pocket of TNF-α-converting enzyme. In still other embodiments of the invention, the associating compound is designed to (i) incorporate a moiety that chelates zinc, (ii) form a hydrogen bond with Leu348 or Gly349 of TNF-α-converting enzyme, (iii) introduce a non-polar group which occupies the S1' pocket of TNF-α-converting enzyme, (iv) introduce a group which

lies within the channel joining S1' - S3' pockets of TNF-α-converting enzyme and which makes appropriate van der Waal contact with the channel, and/or (v) form a hydrogen bond with Leu348 or Gly349 on the backbone amide groups of TNF-α-converting enzyme.

These and other aspects of the invention will become apparent to the skilled artisan in view of the teachings contained herein.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1: Figure 1 is a ribbon diagram of the TACE catalytic domain (TCD). The chain starts on the lower left back side, runs through the structural elements sI, hAI, hA, sII, hB, hB2, sIII, IV, IVa, sIVb, sV, hC, Met-turn and hD, and ends in the upper left back. The three disulfides are shown as connections, with the sulphurs given as small spheres. The catalytic zinc (central sphere) is liganded by the three imidazoles of His4O5, His4O9 and His415, and by the hydroxyl and the carbonyl oxygen atoms of the inhibitor hydroxamic acid group. The inhibitor mimicking interaction of primed-site residues of a peptide substrate is shown in full. Figure 1 was made using SETOR. See Evans, S. "SETOR: Hardware Lighted Three-Dimensional Solid Model Representations of Macromolecules" *J. Mol. Graph.* 11:134-138 (1993).

Figs. 2a and 2b: Figures 2a and 2b are solid surface representations of the catalytic domains of TACE (TCD) (Figure 2a) and MMP-3 (Figure 2b). The electrostatic surface potential is contoured from -15 (intense red) to 15 (intense blue) k_8T/e. Both active-site clefts run from left to right, with the catalytic zinc atoms (spheres) in the centers. In TACE, the bound inhibitor is shown in full structure, binding with its isobutyl (P1') and its Ala (P3') sidechains into the deep S1' and the novel S3' pockets. The orientation is similar to Fig. 1. Figures 2a and 2b were

made using GRASP. Nicolls, A., Bharadwaj, R. and Houig, B., "Grasp - Graphical representation and analysis of surface properties," *Biophys.* 64, A166 (1993).

Fig. 3: Figure 3 aligns the catalytic domain sequences of adamalysin II (ADAM_CROAD), TACE and human ADAM 10 (hADAM1O), according to their topological equivalence and sequence similarity, respectively. The residue numbers are due to the generic TACE numbering. Arrows and braces represent β-strands and α-helices in TACE.

Fig. 4: Figure 4 is a stereo section of the final 2.0 Å electron density around the catalytic zinc (large, central sphere) superimposed with the final TACE model. Visible are the three zinc liganding imidazole rings of His4O5 (top), His4O9 (left) and His415 (bottom), the "catalytic" Glu406, and the hydroxamic acid moiety of the inhibitor. The orientation is similar to Fig. 1. Figure 4 was made using TURBO-FRODO. See Roussel, A. & Cambilleau, C., "Turbo-Frodo in Silicon Graphics Geometry," *Partners Directory*, Silicon Graphics, Mountain View, CA (1989).

Fig. 5: Figure 5 is a superposition of the ribbon plots of the catalytic domain of TACE (light) and adamalysin (dark). Also shown is the catalytic zinc of TACE (sphere) and the three (TACE) and two (adamalysin) disulfide bridges. The orientation is similar to Fig. 1. Figure 5 was made using GRASP.

Fig. 6: Figure 6 illustrates a system for studying a TNF-α converting enzyme, including a video memory storing information for generating a visual display of at least a portion of a TNF-α converting enzyme.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a highly purified tumor necrosis factor-α converting enzyme (TACE) polypeptide, a method of producing and purifying a TACE polypeptide, a method of crystallizing a TACE polypeptide, and a TACE polypeptide crystal. The invention further relates to a X-ray diffraction method using a TACE polypeptide crystal, and to a method of obtaining the X-ray crystallographic structural coordinates of a TACE polypeptide as well as the structural coordinates themselves. Still further, the present invention relates using the structural coordinates of a TACE polypeptide to elucidate the three-dimensional structure of a TACE polypeptide and designing and developing compounds that associate with TACE. Knowledge of the three-dimensional structure and structure coordinates provided according to the invention permit the skilled person to make compounds that will interact with TACE. Such interacting compounds can be made by a variety of techniques and design criteria, including those disclosed in *Protein Engineering* (Oxender and Fox, eds.) (Alan R. Liss, Inc. 1987).

As used herein, TACE refers to a group of polypeptides that are capable of converting the 26 kD cell membrane-bound form of TNFα into the soluble 17 kD form that comprises the C-terminal 156 residues of the TNFα protein. TACE encompasses proteins having the amino acid sequence described in PCT application No. WO 96/41624, herein incorporated in its entirety by reference, as well as any of those proteins having homology, preferably no less than 50%, more preferably at least 80% homology, still more preferably 90% homology to such sequence, at the amino acid level. Additionally, TACE further refers to the expression products of nucleotide sequences disclosed in PCT application No. WO 96/41624. TACE further encompasses the membrane-bound protein and soluble or truncated proteins comprising the extracellular portion of the protein and which retain biological activity and are capable of being secreted. Examples of such proteins are described in PCT application No. WO 96/41624.

The TACE amino acid sequence, or any part or residue thereof, can be found in Black *et al.*, "A Metalloproteinase disintigrin that releases tumour-necrosis factor-α from cells," *Nature* 385: 729-733 (Feb. 1997), herein incorporated in the entirety by reference. Variations in the amino acid sequence of TACE are within the present invention as well. All references to the TACE amino acid sequence contained herein refer to the sequence in Black *et al.*, supra.

As used herein, the TACE catalytic domain (TCD) refers to the portion of a TACE polypeptide between residues 215 and 477 and including the preceding furin cleavage site (residues 211-214), or any part thereof that is capable of cleaving the peptide PLAQAVRSSS.

Expression, Isolation and Purification of TACE Polypeptides

Tumor necrosis factor-α converting enzyme (TACE) is described in the published PCT application No. WO 96/41624. The application describes isolated nucleic acids encoding TACE or portions of TACE, expression vectors comprising a cDNA encoding TACE or portions thereof, and host cells transformed or transfected with the expression vectors comprising a cDNA encoding TACE or portions of TACE. The application further describes processes for producing TACE and portions thereof, for example by culturing transfected cells engineered to express TACE, followed by purification of the recombinantly produced TACE or portion thereof. Methods of isolating, expressing, and purifying a TACE polypeptide are described in detail in published PCT application No. WO 96/41624. The entirety of PCT 96/41624 is incorporated herein by reference.

According to the invention, cDNA encoding the signal peptide, pro and catalytic domains of TACE, *i.e.*, amino acid residues 1-477 is inserted into a suitable expression vector and expressed in a suitable cell line. The cDNA also may include other regions that facilitate expression or achieve other objects that

otherwise that do not depart from the essence of the invention, such as flanking regions.

The cDNAs encoding the TACE polypeptide, or functional portions thereof, such as the TCD, may be altered by addition, substitution, deletion, or insertion. Such alterations may be made, for example, to prevent glycosolation, prevent formation of incorrect or undesired disulfide bridges, and/or enhance expression. Examples of such alterations are described in WO 96/41624 and can be carried out by the methods described therein and other conventional methods. TACE may also be conjugated. Such conjugates may comprise peptides added to facilitate purification and/or identification. Such peptides include, for example, poly-His peptides. Conjugation is described in U.S. Patent No. 5,011,912 and Hopp *et al.*, *Bio/Technology* 6:1204 (1988).

In one embodiment of the invention, the cDNA encodes a TNF-α converting enzyme polypeptide comprising the signal peptide, pro and catalytic domains of TACE (TCD), residues 1-477, with Ser266 changed to Ala and Asn452 changed to Gln. These substitutions are useful in preventing N-linked glycosolation. Additionally, the sequence Gly-Ser(His)$_6$ may be added to the C-terminus. The addition of the sequence Gly-Ser(His)$_6$ facilitates purification of the polypeptide using metal-chelate affinity resins, such as Ni-NTA resins.

Recombinant expression vectors containing the nucleotide sequence encoding TACE, or a portion thereof, may be prepared using well known methods. Suitable host cells for expression of TACE polypeptides include prokaryotic, yeast, and higher eukaryotic cells. Vectors and host cells suitable for use in the present invention are described in WO 96/41624. Further examples of suitable expression systems that can be employed to express recombinant TACE according to the present invention include mammalian or insect host cell culture expression systems, including baculovirus systems in insect cells (See Luckow and Summers, *Bio/Technology* 6:47 (1988))and mammalian cell lines such as COS-7 cells

(Gluzman et al., *Cell* 23:175 (1981)). Additional examples are known in the art and include those described in WO 96/41624. In one embodiment of the invention, the TACE polypeptide is expressed in CHO cells. In this embodiment, the cells secrete a mixture of TACE polypeptide beginning with Val212 and Arg215.

In one embodiment, stable expressing cells may be selected by culturing the cells in a drug that kills those cells that do not incorporate the vector. Examples of suitable selection methods are described in, for example, Kaufman, R.J., "Selection and coamplification of heterologous genes in mammalian cells," *Methods in Enzymology*, 185:537-566 (1990).

Purification of the expressed TACE polypeptide may be carried out by any suitable means, such as those described in WO 96/41624. According to one aspect of the invention, it is preferable to obtain a TACE polypeptide that is suitable for crystallization. In obtaining a TACE polypeptide suitable for crystallization, it is important that the process for purifying the TACE polypeptide is sufficient to yield a polypeptide pure enough to properly crystallize.

A preferred method of purification starts with a suitable amount of medium from the culture of TACE-secreting cells. This medium is generally a supernate of the culture. The medium contains the TACE polypeptide to be purified. Preferably, the TACE polypeptide is recombinantly produced using DNA coding for the TACE polypeptide with the sequence altered to encode a conjugate or conjugates that facilitate purification. For example, the sequence encoding Gly-Ser-$(His)_6$ may be added to the C-terminus to facilitate purification using metal-chelate resins.

The medium is concentrated, for example, by diafiltration. Suitable diafiltration units include a Millipore 10K cut-off, 1 ft^2 TFF diafiltration unit. A suitable buffer solution is then added to the concentrated medium. Any suitable buffer may be used. One such suitable buffer contains 20 mM Tris (pH 7.5) and 300 mM NaCl.

The sample is reconcentrated and diluted numerous times. For example, the sample may be reconcentrated and diluted a second time with the buffer, reconcentrated again, diluted a third time with the buffer, and reconcentrated a final time. The sample retained in the diafiltration unit is recovered by a suitable method, such as by a back-flush method. The recovered material may then be filtered through a suitable membrane. Suitable membranes include, for example, 0.45 or 0.22 micron pore-size membranes. Azide is then added. The filtered sample may then be stored overnight at a low temperature, such as about 2-9 °C. After overnight storage, imidazole from a stock solution in water and $ZnCl_2$ from a stock solution in water are added to the filtered sample. The sample then is pumped over a suitable column. One suitable column, particularly when the TACE polypeptide is conjugated with the sequence Gly-Ser-$(His)_6$, is a metal-chelate resin, such as a Ni-NTA resin.

The column is washed with a buffer, such as a buffer of 20 mM Tris pH 7.5, 300 mM NaCl, 5 mM imidazole, and 5 uM $ZnCl_2$. The TACE polypeptide is then eluted with an increasing gradient of imidazole. Fractions are collected in tubes containing glycerol in water Tris pH 8. Preferably, the glycerol solution is prepared the day of the column run.

An aliquot from each fraction is spotted on a membrane which is stained with amido black to determine which fractions contain a significant amount of protein. Alternatively, a small amount, for example 5 μl, from each fraction may be used for gel analysis using Coomassie staining. The fractions with a significant amount of protein are pooled, and the pool is then concentrated with, for example, a diafiltration unit.

In some cases, aggregation of polypeptide may occur. In order to eliminate aggregates and further facilitate purification, an inhibitor of TACE, such as a hydroxamate-based inhibitor, may be added to the concentrated sample from a stock solution in water, and octylglucoside (commercially available from Boehringer

Mannheim) is added from a stock solution in water. The sample is then incubated at room temperature for 15-24 hours.

Following incubation, the sample is applied to a size exclusion column. The column is first equilibrated with a suitable buffer, such as a buffer of 10 mM Tris pH 7.5, 100 mM NaCl, 10% glycerol. Suitable size exclusion columns include, for example, LKB 2135-365, packed with TSK-G3000 SWG or the like such as Superdex-200. The buffer is then pumped through the column. The highly purified TACE polypeptide can be detected by absorption at 280 nm.

A gel analysis of all fractions with significant protein is carried out to determine which fractions should be pooled. The size exclusion chromatography pool is concentrated using, for example, a diafiltration unit.

A binding partner, such as an inhibitor, may then be added to the purified sample. The binding partner is particularly useful in stabilizing the TACE polypeptide. The binding partner may be any suitable compound. Suitable binding partners include, for example, hydroxamate-based inhibitors. One suitable inhibitor is N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine, 2-(amino)ethyl amide. This inhibitor, as well as other inhibitors, are described in US patent No. 5,594,106 (Black *et al.*), herein incorporated in its entirety by reference.

The protein complex can be stored at low temperature, for example, at about 4 °C.

TACE Crystal and Methods of Crystallization of TACE Polypeptides

One aspect of the invention relates to a method of crystallizing a TACE polypeptide. A preferred method comprises co-crystallizing a TACE polypeptide with a binding partner described above. Exemplary means for obtaining the TACE polypeptide, as well as purification of the polypeptide are described above.

Crystals may be grown or formed by any suitable method, including drop vapor diffusion, batch, liquid bridge, and dialysis, and under any suitable conditions. Crystallization by drop vapor diffusion is often preferable. In addition, those of skill in the art will appreciate that the crystallization conditions may be varied. Various methods of crystallizing polypeptides are generally known in the art. See, for example, WO 95/35367, WO 97/15588, EP 646 599 A2, GB 2 306 961 A, and WO 97/08300.

In one embodiment of the invention, a DNA construct comprising TACE residues 1-477, with Ser266 changed to Ala, Asn452 changed to Gln, and the sequence Gly-Ser-$(His)_6$ added to the C-terminus, may be expressed in CHO cells. These cells primarily secrete a processed mixture of TACE, about half beginning with Val212 and about half with Arg215. The mixture is purified as described above. The purified TACE polypeptide, with the added binding partner, is stored in a buffer as described above.

The TACE polypeptide and binding partner are co-crystallized. The TACE/binding partner solution, at a polypeptide concentration of about 5 mg/mL to about 12 mg/mL in a TACE buffer described above, is mixed with a suitable crystallization buffer and crystallized using a suitable crystallization technique, for example drop vapor diffusion. Suitable crystallization buffers, for example, include: 0.1 M Na Acetate pH 5.3, 0.2 M $CaCl_2$, 30% v/v Ethanol; 0.1 M Na Citrate pH 5.0, 40% v/v Ethanol; 0.1 M Na Citrate pH 8.7, 20% w/v PEG 4000, 20% v/v Isopropanol; and 0.1 M Na Citrate pH 5.4, 20% w/v PEG 4000, 20% v/v

Isopropanol. The sample is incubated at a temperature ranging from about 4 to 20 degrees Celsius. A crystalline precipitate is formed.

Seeds from the crystalline precipitate obtained, as whole crystals or crushed crystal suspensions, are transferred, along with a suitable crystallization promoter, such as hair of rabbit, to a solution of concentrated TACE/substrate in a crystallization buffer. Crystals suitable for X-ray data collection are formed.

Another aspect of the invention relates to a TACE polypeptide crystal. One such crystal comprises a TNF-α converting enzyme catalytic domain (TCD) polypeptide co-crystallized with an inhibitor. The crystal diffracts to about 2 A and belongs to the monoclinic space group $P2_1$. The crystal's unit cell comprises four crystallographically independent TCD molecules. The TCD molecules are in an asymmetric unit and are not clustered into separate tetrameres, but are integrated into the infinite periodic structure. The crystal has the cell constants: a=61.38 Å (angstrom), b=126.27 Å, C=81.27 Å and β=107.41°.

X-Ray Diffraction

Another aspect of the invention relates to the structure of TACE, particularly the structure of the TACE catalytic domain (TCD). The structure of TACE can be determined utilizing a crystal comprising a TACE polypeptide as described above. According to the present invention, the structure of TACE, and particularly the TCD, is determined using X-ray crystallography. Any suitable X-ray diffraction method for obtaining three-dimensional structural coordinates of a polypeptide may be used. The three-dimensional structure coordinates, or any part thereof that characterizes the part of the TACE polypeptide of interest, such as the TACE catalytic domain or part thereof that is capable of cleaving the peptide PLAQAVRSSS, can be used as described herein.

Methods of Using TACE X-Ray Diffraction Coordinates

The invention also relates to use of the structure coordinates obtained from the above described X-ray diffraction studies of the TACE catalytic domain. The coordinates may be utilized, by direct analysis, with the aide of computers, or combinations thereof, to determine the structure, including secondary and tertiary structure, of the TACE catalytic domain. The TACE catalytic domain structure coordinates also may be used to develop, design, and/or screen compounds that associate with TACE. As used herein, "associate" means that the compound may bind to or interact with TACE ionically, covalently, by hydrogen bond, van der Waals interaction, salt bridges, steric interaction, hydophilic interactions and hydrophobic interaction. Moreover, the term "associate" encompasses associations with any portion of the TACE catalytic domain. For example, compounds that associate with TACE may be compounds that act as competitive inhibitors, un-competitive inhibitors, and non-competitive inhibitors. Compounds that associate with TACE also may be compounds that act as mediators or other regulatory compounds. Compounds that associate with TACE also may be compounds that isomerize to short-lived reaction intermediates in the chemical reaction of substrate with TACE. In particular, compounds designed to associate with TACE may be used therapeutically as inhibitors, mediators and other regulatory compounds.

The use of X-ray coordinates for structure determination, molecular design and selection and synthesis of compounds that associate with other polypeptides is known in the art. Published PCT application WO 95/35367 describes the use of X-ray structure coordinates to design, evaluate, synthesize and use compounds that associate with the active site of an enzyme. UK Patent Application 2306961A describes the use of X-ray coordinates in rational drug design. Published PCT application, WO 97/15588 describes the structural determination of a polypeptide using x-ray diffraction patterns as well as use of the coordinates and three-dimensional structure in finding compounds that associate with the polypeptide of

interest. This invention, however, for the first time allows the use of X-ray coordinates for a TACE polypeptide for structural determination, molecular design, and selection and synthesis of compounds that associate with TACE.

In one aspect of the invention, the structure coordinates obtained by the foregoing methods may be displayed as, or converted to, a graphical representation, including three-dimensional shape representations. This may be accomplished using commercially available computer programs capable of generating graphical representations of molecules, or parts thereof, from a set of structural coordinates. Examples of computer programs capable of generating graphical representations of molecules, or parts thereof, from a set of structural coordinates are described in published PCT application WO 97/08300, incorporated in the entirety by reference.

In another aspect of the invention, the structure coordinates and structure may be compared to, or superimposed over, other similar molecules, such as other metalloproteinases. For example, the TACE structure coordinates and structure may be compared to or superimposed over the structure coordinates or structure of snake venom metalloproteinases, such as, for example, adamalysin II. The TACE structure coordinates and structure also may be compared to or superimposed over the structure coordinates or structure of matrix metalloproteinases, such as ADAM 10, including human ADAM 10. Comparison of TACE and other molecules for which a graphical structure or three-dimensional structural coordinates are available may be carried out with the aide of available software applications, such as the Molecular Similarity application of QUANTA (Molecular Simulations, Inc., Waltham, MA).

Compounds that associate with TACE also may be computationally evaluated and designed by screening and selecting chemical entities or fragments for their ability to associate with TACE, and specifically the TACE catalytic domain. Several methods may be used to accomplish this aspect of the invention. In one embodiment, one may visually inspect a computer-generated model of TACE, and

specifically the catalytic domain, based on the structure coordinates described herein. Computer generated models of chemical entities or specific chemical moieties can then be positioned in or around the catalytic domain and evaluated based on energy minimization and molecular dynamics, using, for example, available programs such as CHARMM or AMBER. Positioning of the chemical entity or fragment can be accomplished, for example with docking software such as Quanta and Sybyl. Additionally, known and commercially available computer programs may be used in selecting chemical entities or fragments. Once suitable chemical entities or fragments are selected, they may be assembled into a single compound, such as an inhibitor, mediator, or other regulatory compound. Known and commercially available model building software may assist in assembly.

In one aspect of the invention, compounds that associate with TACE and specifically the TACE catalytic domain may be designed as a whole, rather than by assembly of specific chemical moieties or chemical entities. This embodiment may be carried out using computer programs such as LUDI (Biosym Technologies, San Diego, CA), LEGEND (Molecular Simulations, Burlington, MA), and Leap Frog (Tripos Associates, St. Louis, MO).

In one embodiment, a candidate compound is chosen based upon the desired sites of interaction with TACE and the candidate compound in light of the sites of interaction identified previously. Once the specific candidate compound-TACE interactions are determined, docking studies, using commercially available docking software, are performed to provide preliminary "modeled" complexes of selected candidate compound with TACE.

Constrained conformational analysis is performed using, for example, molecular dynamics (MD) to check the integrity of the modeled TACE-inhibitor complex. Once the complex reaches its most favorable conformational state, the structure as proposed by the MD study is analyzed visually to ensure that the modeled complex complies with known experimental SAR/QSAR (structure-activity

relationship/quantitative structure-activity relationship) based on measured binding affinities.

Other modeling techniques also may be used in accordance with the invention. Examples of these techniques are disclosed in Cohen *et al.*, "Molecular Modeling Software and Methods for Medicinal Chemistry," *J. Med. Chem.*, 33:883-894 (1990) and Navia *et al.*, "The Use of Structural Information in Drug Design," *Current Opinions in Structural Biology*, 2:202-210 (1992), herein incorporated by reference in the entirety.

Compounds developed or designed to associate with TACE may be optimized or the efficiency of association can be tested using a number of methods known in the art. For example, the deformation energy and electrostatic interactions may be determined and optimized. Known and commercially available software and hardware systems may be used. Examples of such software are disclosed in WO 95/07619. Structure-based analoging for optimization of the inhibitor potency, selectivity and physical drug-like properties in an iterative manner also may be performed by one skilled in the art of drug design.

Substitutions also may be made to selected or designed compounds. These substitutions can be made to improve or modify the association properties of the compound. Such substitutions may be made, for example, in side groups or particular atoms of the compounds. Generally, one should begin with conservative substitutions that have approximately the same size, shape, charge and other characteristics of the original group or atom. Substituted compounds may be further analyzed and optimized as described above.

In a further aspect of the invention, the potential inhibitory, mediatory, regulatory, or other binding effect of a compound may be analyzed and evaluated, using, for example, commercially available computer software, prior to actual synthesis and testing of such compound. In this way, one can evaluate the probability of synthesizing and testing of inoperative compounds.

Procedures for measuring inhibition generally are known in the art and are disclosed, for example, in PCT 96/41624. Such methods include assays based on reaction with a peptide substrate.

TACE Catalytic Domain Structure

The physical features of the TCD, determined based on the X-ray diffraction data obtained using the methods described and its use in creating molecular models of the TCD, are further described, with reference to the Figures.

The domain depicted in Fig. 1 has the shape of an oblate ellipsoid, notched at its flat side to give a relatively small active-site cleft separating the small "lower" subdomain from the "upper" main molecular body (Fig. 2a). The TCD polypeptide chain starts on the molecular surface (in the lower back, Fig. 1), with the chain becoming well defined between Asp217 and Met221 (see Fig. 3). Central to the molecule is the five-stranded β-pleated sheet, with the β-strands arranged in the order (from back to front, see Fig 1) sII, sI, sIII, sV and sIV (see Fig. 3), with sIV, the "edge" strand, running antiparallel to the others. This β-sheet is highly twisted flanked by two α-helices (hB and hB2) on its convex and two helices (hA and hC) on its concave side. The β-strands sI and sII are connected by the short α-helix hA1 and the long α-helix hA (the obliquely running helix on the backside, Fig. 1). The β-strands sII and sIII are linked by the large "multiple-turn loop", the long "intermediate" α-helix hB and the adjacent short α-helix hB2, all of them arranged on "top" of the β-sheet thus fully shielding its central part from bulk water (Fig. 1). The multiple-turn loop is bulged out at two sites giving rise to a "spur-like" and a quite acidic protuberance, respectively (visible in Fig. 2a on top of the molecule). The sIII-sIV linker terminates in a short "bulge", before it enters the edge strand sIV. The sIV-sV connecting segment is dissected into two large "ear-like" surface-located loops, a first one nestling to the main molecular body (giving rise to the "blue" surface, center left, in Fig. 2a), and a long β-hairpin loop (sIIa-sIIb)

projecting from the molecular surface (top left in Figs. 1 and 2). A bulged-out loop links sV with the "active-site helix" hC, which is located in the center of the molecule and stops abruptly at the strictly conserved Gly412, where the chain kinks down to build the lower subdomain.

The C-terminal chain comprising the last 61 TCD residues (Fig. 3) first forms three short straight almost perpendicularly arranged segments linked by two "narrow" supertwisted loops, returns via the tight "Met-turn" Tyr433-Val434-Met435-Tyr436 back to the surface where it kinks at Pro437 to form the Pro437-Ile438- Ala439 outer "wall" of the S1' crevice, approaches in a wide loop the C-terminal α-helix hD and runs through it, and ends up on the molecular "back" surface close to the N-terminus, with the last defined residues Arg473-Ser474 fixed via hydrogen bonds to the main molecular body. Via Cys423-Cys453, the first of the two "narrow" loops is disulfide-linked with the N-terminus of helix hD, whose C-terminal end in turn is clamped to the "ear-like" sIV-sV linker peptide through Cys365-Cys469. Spatially adjacent, the third disulfide bridge of TCD, Cys225-Cys333, connects the N-terminal parts of β-strands sI and sIII. In the intact TACE molecule, four residues downstream of Ser474 would reside Cys478, which is already integral part of the compact elongated disintegrin domain (Saudek *et al.*, "Three-dimensional structure of echistatin, the smallest active RGD protein" *Biochem.* 30, 7369-7372 (1991)). Considering Ser474 and this Cys478 as pivot points of their respective domains, the three residue linker would allow relatively unconstrained docking of the disintegrin domain to the "left" surface side of the catalytic domain.

The active-site cleft of TACE (Fig. 2a) is relatively flat on the left hand (non-primed) side, but becomes notched towards the right. The catalytic zinc residing in its center is penta-coordinated by the three imidazole N$\in$2 atoms of His4O5, His4O9 and His415 (provided by the active-site helix and the following ''descending'' chain comprising the conserved zinc binding consensus motif

HEXXHXXGXXH), and by the carbonyl and the hydroxyl oxygen of the hydroxamic acid moiety of the inhibiter (see Figs. 1, 2a and 4). This zinc-imidazole ensemble is based on the distal ∈-methyl-sulphur moiety of the strictly conserved Met435, harbored in the Met-turn characteristic for the metzincin clan (Bode *et al.*, "Astacins, serralysins, snake venom and matrix metalloproteinases exhibit identical zinc binding environments (HEXXHXXGXXH and Met-turn) and topologies and should be grouped into a common family, the 'metzincins'" *FEBS Lett.* 331, 134-140 (1993); Stöcker *et al.*, "The metzincins: Topological and sequential relations between the astacins, adamalysins, serralysins, and matrixins (collagenases) define a superfamily of zinc-peptidases" *Protein Sci.* 4, 823-840 (1995)). Both carboxylate oxygens of the "catalytic" Glu4O6 (which acts as a general base during catalysis (Grams *et al.*, "X-ray structures of human neutrophil collagenase complexed with peptide hydroxamate and peptide thiol inhibitors: Implications for substrate binding and rational drug design" *Eur. J. Biochem.* 228, 830-841 (1995)) squeezed between the zinc-liganding imidazole of His4O5 and the edge strand, are hydrogen bonded to the hydroxyl and the N-H group of the hydroxamic acid (see Fig.4). To the right of the catalytic zinc opens the deep S1' pocket, which, besides the S1' wall-forming segment (bottom, Figs. 1 and 2a), is bordered by the side chains of His4O5 and Glu4O6 (left), the sIV main chain and the Leu345 side chain (top), and the side chains of Val44O (back) and Ala439 (right). To the right of Ala439 opens a second (S3') pocket, which inside the molecule merges with the S1' pocket, leaving a small bridge made of the opposing side chains of Ala439 and Leu348 (Fig. 2a).

The (pseudo)peptidic part of the inhibitor binds in an extended geometry to the notched right-hand side of the active-site cleft, mimicking the interaction of the primed residues of a productively bound peptide substrate (Fig. 2a). It runs antiparallel to the upper short bulge Gly346-Thr347-Leu348 and parallel to the S1' wall-forming segment Pro437-Ile438-Ala439, making two and two inter-main chain

hydrogen bonds, respectively. The dominant intermolecular interactions are made by the P1' isobutyl (pseudo-leucyl) side chain of the inhibitor and the essentially hydrophobic S1' pocket, however, is large and accommodates three partially ordered solvent molecules in addition. The P2' t-butyl side chain extends away from the enzyme, but nestles to the hydrophobic canopy above formed by the enzyme's bulge. The P3' Ala side chain points into the large negatively charged S3' pocket, but is too short to make favorable contacts. The C-terminal diaminoethyl group has different conformations in the four molecules.

The P1' to P3' segment Val77-Arg78-Ser79 of a bound pro-TNFα probably binds in a similar manner, possibly under better matching with the underlying cleft surface; the preceding P3 to P1 residues Ala74-Gln75-Ala76 certainly will align antiparallel to the edge strand, with their side chains extending into the (partially charged) S3 pocket and the (negatively charged) shallow S2 depression, and projecting out of the central cleft, respectively. The primed subsites and surrounding molecular surfaces of TACE are dominated by negative charges, while the non-primed subsites are essentially hydrophobic in nature (Fig. 2a). More distant interactions may be involved in the specificity of TACE for processing pro-TNFα. The 12 residue substrate comprising the pro-TNFα cleavage site can also be split by some of the MMPs, although with less specificity and efficacy (Black *et al.*, "Relaxed specificity of matrix metalloproteinases (MMPs) and TIMP intensity of tumor necrosis factor-α (TNF-α) production suggest the major TNF-α converting enzyme is not an MMP" *Biochem. Biophys. Res. Commun.* 225, 400-405 (1996)). Thus, the preferential processing of the (probably trimeric) (Tang *et al.*, "Human pro-tumor necrosis factor is a homotrimer" *Biochem.* 35, 8216-8225 (1996a); Tang *et al.*, "Length of the linking domain of human pro-tumor necrosis factor determines the cleavage processing" *Biochem.* 35, 8226-8233 (1996b)) membrane-bound pro-TNFα in *vivo* might in part be due to correct assembling, i.e. suitable presentation of the pro-TNFα cleavage segment to the TACE active site in a distinct distance

from the anchoring membrane. Some experimental evidence (Tang *et al.*, *Biochem.* 35, 8216-8225 (1996a); Tang *et al.*, *Biochem.* 35, 8226-8233 (1996b)) suggests that the cleavage site might not be determined by the cleavage sequence alone, but that also the distance to the base of the compact cone formed by the associated C-terminal segments of three TNFα molecules (Jones *et al.*, "Structure of tumor necrosis factor" *Nature* 338, 225-228 (1989)) plays a role. In a productive TACE-proTNFα complex, the base of this TNFα-trimer cone (into which the disordered N-termini run up) may be recognized by the "right" side of the TACE catalytic domain (Fig. 2a), with the about 10 residues long spacer favoring the correct placement of the proTNFα Ala76-Val77 scissile peptide bond in the active site of TACE.

The polypeptide topology and in particular the surface presentation of the catalytic zinc prove the catalytic domain of TACE to be a typical metzincin. (Bode *et al.*, "Astacins, serralysins, snake venom and matmrix metalloproteinases exhibit identical zinc binding environments (HEXXHXXGXXH and Met-turn) and topologies and should be grouped into a common family, the 'metzincins'" *FEBS lett.* 331, 134-140 (1993); Stöcker *et al.*, "The metzincins: Topological and sequential relations between the astacins, adamalysins, serralysins, and matrixins (collagenases) define a superfamily of zinc-peptidases" *Protein Sci.* 4, 823-840 (1995)) A superposition with the other metzincins shows, however, that its topology is most similar to that of the catalytic domain of snake venom metalloproteinases such as adamalysin II (Fig. 5). (Gomis-Rüth *et al.*, "First structure of a snake venom metalloproteinase: prototype for matrix metalloproteinases/collagenases" *EMBO J.* 12, 4151-4157 (1993); Zhang *et al.*, "Structural interaction of natural and synthetic inhibitors with the venom metalloproteinase, atrolysin C (form d)" *Proc. Natl. Acad. Sci. USA* 91, 8447-8451 (1994); Kumasaka *et al.*, "Crystal structure of H2-proteinase from the venom of Trimeresurus flavoviridis" *J. Biochem.* 119, 49-57 (1996)) This close homology is

reflected by the much better simultaneous superposition of the central sheet and the large helices, but in particularly also by a couple of structural features, which TACE shares exclusively with the adamalysins such as: the long helix hB and the preceding multiple-turn loop arranged on top of the β-sheet; the typically arranged and shaped C-terminal helix hC; and the extended C-terminus placed on the backside surface. About 175 of the 263 TACE and 201 adamalysin α-atoms are topologically equivalent (with an rms deviation of 1.3 Å, 39 of which have identical side chains (Fig. 3). These numbers are close to those obtained from a comparison of members within the different metzincin families. (Stöcker *et al.*, *supra*) In addition, detailed structural features prove the close relationship of TACE to the adamalysins: a more conserved core structure; the loosely arranged N-terminus; the characteristic Asp416 (directly following the zinc binding consensus motif, Fig. 3) involved in identical intramolecular hydrogen bond interactions; the adjacent disulfide bridge Cys423-Cys453 linking the first narrow loop to the C-terminal helix hD (which TACE does not share with adamalysin II, but with the H2-proteinase from the snake venom of T. flavoviridis) (Kumasaka *et al.*, *supra*); disulfide bridge Cys365-Cys469 connecting the sIV-sV linker with the C-terminal helix hD; a similarly shaped active-site cleft, with particularly strong similarities in the SI' pocket and other primed subsites.

The catalytic domain of TACE (TCD) also differs from adamalysin II in several respects: with 263 residues, its chain is much longer; most of the additional residues of TACE are clustered giving rise to a more projecting hA-sII turn, to the two surface protuberances of the multiple-turn loop, to the two "ears" of the sIV-sV linker, and to a more bulged-out sV-hC connector (see Figs. 3 and 5); lack of a calcium binding site but presence of a third disulfide bridge Cys225-Cys333 in TACE, both elements serving, however, for the same function namely to clamp the N- terminal chain to strand sill; the quite deep S3' pocket of TACE which merges

with its S1' pocket; an almost inverted charge pattern in and around the primed subsites, with an absolute predominance of positive charges in adamalysin.

According to its sequence, and probably with respect to its three-dimensional structure, the TACE catalytic domain is thus not a typical member of the mammalian ADAMs proper (a family of membrane-anchored cell-surface proteins, with the catalytic domain quite homologous to adamalysin (Wolfsberg *et al.*, "ADAMs in Fertilization and Development" *Developm. Biol.* 180, 389-401 (1996))) TACE presumably shares this "outsider" role with (bovine) ADAM 10 (Fig. 3), which does also possess some TACE-like activity (Lunn *et al.*, "Purification of ADAM 10 from bovine spleen as a TNFα convertase," *FEBS Lett.* 400, 333-335 (1997)), and whose *Drosophila* version *(kuz)* has recently been shown to process the Notch receptor (Rooke *et al.*, *Science* 273, 1227-1231 (1996)). Also ADAM 10 probably exhibits an elongated hA-sII loop and the two "ears" typical for TACE, but might have a multiple-turn intermediate in size between TACE and adamalysin (see Fig. 3). Ninety of the ADAM 10 catalytic domain residues are identical to TACE further underlining the close homology (see Fig. 3), whereas the other mammalian ADAMs probably resemble much more adamalysin II (Gomis-Ruth *et al.*, "Refined 2.0 A crystal structure of snake venom zinc endopeptidase adamalysin II" *J. Mol. Biol.* 239, 513-544 (1994)).

The structural homology of TACE to the MMPs is significantly lower. The relative arrangement of the common secondary structural elements differs more (reflected by the significantly larger rms deviation of 1.6 Å of the about 120 topologically equivalent Cα-atoms), and the MMPs lack characteristic TACE/adamalysin structural elements (such as the intermediate helix hB and the multiple-turn loop, the Asp residue behind the third zinc-binding histidine), or exhibit typical determinants (such as the structural zinc and the integrated calcium ions) not seen in TACE. Notwithstanding the differences in secondary structure, the active-site cleft of TACE bears some similarity with that of the MMPs, with the

flat nonprimed (left-hand) side, and the narrow primed side centering in the deep S1' pocket (Fig. 2b). This subsite similarity to the MMPs explains the observed partial sensitivity of TNFα-convertase activity towards synthetic hydroxamic acid inhibitors originally designed for inhibition of various MMPs (DiMartino *et al.*, "Anti-arthritic activity of hydroxamic acid-based pseudopeptide inhibitors of matrix metalloproteinases and TNFα processing" *Inflamm. Res.* 46, 211-215 (1997)). Model building experiments with TIMP-1 structure (Gomis-Rüth *et al.*, "Mechanism of inhibition of the human matrix metalloproteinase stromelysin-1 by TIMP-1" *Nature* 389, 77-81(1997)) show no obvious obstacles in the active-site region of TACE that would easily explain its resistance to blockage by the TIMPs.

This TCD crystal structure thus gives evidence for a topological similarity of the catalytic domain of TACE with that of the adamalysins/ADAMs, and for a share of its substrate binding site to that of the MMPs. TACE exhibits, however, several structural peculiarities regarding surface contour, charge and shape, which facilitates the design of potent selective synthetic inhibitors.

In designing and developing compounds, such as inhibitors, mediators and other compounds having activities with biological significance, that associate with TACE, it is desirable to select compounds with a view toward the particular surface contour, charge, shape, and other physical characteristics of the TACE catalytic domain. Generally, the compounds should be capable of physically and structurally associating with TACE, as well as be able to assume a conformation that allows it to associate with TACE. The features described above will direct the skilled artisan in this regard. In particular, compounds with a linear functionality should be particularly suitable. Such compounds will be particularly suitable in light of the deep pockets of the TACE catalytic domain.

The compounds that associate with TACE, for example, may be designed to associate with the S1' region or the S1'S3' pocket of TACE. Compounds that associate with TACE also may be designed to (i) incorporate a moiety that chelates

zinc. Further exemplary compounds include compounds are designed to form a hydrogen bond with Leu348 or Gly349 of TACE, (ii) introduce a non-polar group which occupies the S1' pocket of TACE, (iii) introduce a group which lies within the channel joining S1' - S3' pockets of TACE and which makes appropriate van der Waal contact with the channel, and (iv) form a hydrogen bond with Leu348 or Gly349 on the backbone amide groups of TNF-α-converting enzyme, or (v) any combination of the above.

Computer-Readable Medium

The present invention also relates to a computer-readable medium having recorded thereon the x-ray diffraction structure coordinates of a crystalline TACE polypeptide. The computer-readable media of the invention are useful for storage, transfer, and use with software of the TACE structural coordinates. The computer readable medium may be any suitable data storage material, including, but not limited to, a floppy disc, a hard disc, computer-type Random Access Memory, Read-Only Memory flash memory, CD-ROM, recordable and rewritable CDs, recordable and rewritable DVDs, magnetic-optical disk, ZIP drive, JAZ drive, Syquist drive, digital tape drive, or the like. Other suitable media will be known to those of skill in the art.

In one embodiment, the computer readable medium comprises the coordinates of Table 1 or a substantial portion thereof. The computer-readable medium may be used in conjunction with a machine programmed with instructions for using the data recorded on the medium, such as a computer loaded with one or more programs identified throughout the specification, to display a graphical, three-dimensional representation of a TACE polypeptide, or any part thereof.

Computer Based System

Figure 6 illustrates a system 1000 for studying a TACE polypeptide. The system includes a video memory 110 that stores information representing at least a portion of a TACE polypeptide. The memory has at least one first-type storage region 112, having recorded thereon a set of spatial coordinates specifying a location in a three dimensional space, and at least one second-type storage region 114, having recording thereon information representing a characteristic of one of a plurality of amino acids. The second-type storage regions are logically associated with the first-type storage regions in the video memory 110 to represent a geometric arrangement of at least one characteristic of at least a portion of the TACE polypeptide in the three dimensional space. Memory, 112 and 114 can comprise, for example, the data shown in Table 1. The system 1000 also includes a processor, coupled to the memory to access the first-type storage regions 112 and the second-type storage regions 114, to generate image signals for depicting a visual three dimensional image of at least one characteristic of at least a portion of the TACE polypeptide in the three dimensional space based on data from the memory 110. The processor can be any general purpose processor with a CPU, register, memory and the like. A display 130 coupled to the processor 120 via lines 125 to receive the image signals, for depicting a visual three dimensional image of at least one characteristic of at least a portion of the TACE polypeptide in the three dimensional space based on the image data on a screen 132.

In one embodiment of the invention, the image data includes data for depicting a visual three dimensional image of a ribbon structure of at least a portion of a TACE polypeptide in three dimensional space, such as shown in Fig. 1. In another embodiment, the image data includes data for depicting a visual three dimensional image of a solid model representation of at least a portion of said TACE polypeptide in three dimensional space, such as shown in Fig. 2. In still another embodiment, the image data includes data for depicting a visual three

dimensional image of electrostatic surface potential of at least a portion of TACE polypeptide in three dimensional space, such as shown in Fig. 2. In yet another embodiment, the image data includes data for depicting a visual three dimensional stereo image of at least a portion of a TACE polypeptide in three dimensional space, such as shown in fig. 4.

The system 1000 of the present invention may further comprise a storage device 145 that stores data representing a geometric arrangement of a characteristic of a composition other than the TACE polypeptide and an operator interface, such as a mouse 135, for receiving instructions from a operator. Storage device 145 can include, for example, the three-dimensional X-ray coordinate data for other chemical entities. The processor 120 is coupled to the storage device 145 and to said operator interface 135 and generates additional image data for depicting the geometric arrangement of the characteristic of the composition relative to said visual three dimensional image of said at least one characteristic of said at least a portion of TACE polypeptide on the screen 132 based on instructions from the operator interface. In the Fig. 6 embodiment, the storage device 145 is part of the memory 110.

The first-type storage regions 112 and said second-type storage regions 114 are regions of, for example, a semiconductor memory, regions of an optical disk, or regions of a magnetic memory.

In one embodiment, processor 120 and video memory 110 are in the form of a UNIX or VAX computer, such those available from Silicon Graphics, Sun Microsystems, and IBM. However, the invention is not limited to use of this particular hardware and software.

The invention is described in more detail in the following illustrative examples. Although the examples may represent only selected embodiments of the

invention, it should be understood that the following examples are illustrative and not limiting.

Example 1 - TACE Polypeptide Expression, Isolation, and Purification

A cDNA encoding the signal peptide, pro and catalytic domains of TACE, amino acid residues 1-477, as disclosed in Black et al., "A Metalloproteinase disintigrin that releases tumour-necrosis factor-α from cells," *Nature* 385: 729-733 (Feb. 1997), with Ser266 changed to Ala, Asn452 changed to Gln and the sequence Gly-Ser-$(His)_6$ added to the C-terminus, was inserted into an expression vector for CHO cells. The TACE polypeptide was expressed in CHO cells and a mixture of the TACE polypeptide beginning either with Val212 or Arg215 was secreted. The cells were cultured in the drug, methotrexate, which kills those cells that did not incorporate the vector.

The expressed TACE polypeptide was then purified. Purification started with 5 liters of the medium containing the expressed TACE polypeptide. The medium was concentrated to about 200 mL with a Millipore 10K cut-off, 1 ft^2 TFF diafiltration unit. The pumping rate was 50-100 mL/min. Two liters of a buffer solution of 20 mM Tris (pH 7.5) and 300 mM NaCl (Buffer E) was then added to the sample.

The sample was reconcentrated as described above and diluted a second time with 2 liters of Buffer E, reconcentrated again, diluted a third time with 2 liters of Buffer E, and reconcentrated to about 100 mL. The sample retained in the diafiltration unit was recovered by a back-flush. This material was then filtered through a 0.45 µm and was azide added to 0.05%. The filtered sample was stored overnight at 4 °C.

After overnight storage, imidazole was added to the filtered sample to 5 mM from a 200 mM stock in water and $ZnCl_2$ was added to 5 uM from a 1 M stock in

water. The sample then was pumped over 2.2 mL of Qiagen Ni-NTA Superflow resin (Cat. # 30430) at 3 mL/min (column size 7.5 x 50 mm).

The column was washed at 5 mL/min with 100 mL of a buffer of 20 mM Tris pH 7.5, 300 mM NaCl, 5 mM imidazole, and 5 uM $ZnCl_2$ (Buffer A). The protein was then eluted with an increasing gradient of imidazole, going up to 200 mM in 1 minute (5 mL total volume), followed by 35 mL of 200 mM imidazole in Buffer A. Two mL fractions were collected, TACE generally coming off about 6 mL into the elution. The fractions were collected in tubes containing 500 ul of 50% glycerol in water and 200 ul of 1 M Tris pH 8. The glycerol in water was prepared the day of the column run.

A dot blot, with 3 μl from each fraction, was stained with amido black to determine which fractions contained a significant amount of protein. The fractions with a significant amount of protein were pooled. The pool was then concentrated to 1-2 mL with a 10 K cut-off Amicon Centriprep concentrator.

The inhibitor N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine, 2-(amino)ethyl amide was added to the concentrated sample to 1 mM from a 50 mM stock in water, and octylglucoside was added to 1% from a 10% stock in water. The sample was then incubated at room temperature for 15-24 hours.

Following incubation, the sample was applied to a 21.5 x 600 mm size exclusion column, LKB 2135-365, packed with TSK-G3000 SWG, and equilibrated with 10 mM Tris pH 7.5, 100 mM NaCl, 10% glycerol. This buffer was then pumped through the column at 2.5 mL/min for 100 minutes. The TACE polypeptide in the effluent was detected by absorption at 280 nm. Excluded material generally eluted at about 38 minutes. The pure TACE generally eluted at about 78 minutes or longer.

A gel analysis, with 15 μl of all fractions with significant protein was then carried out to determine which fractions should be pooled. The size-exclusion

chromatography pool was concentrated to about 1 mL with a 10 K cut-off Amicon Centriprep concentrator.

The inhibitor N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine, 2-(amino)ethyl amide was then added to the purified sample to a concentration of 1 mM. The protein can be stored at 4 °C.

Example 2 - Protein Crystallization

A DNA construct comprising the prodomain and the catalytic domain of human TACE (resides 1-477) was fused to the sequence Gly-Ser-$(His)_6$ to facilitate purification of the protein on a Ni-NTA affinity column. Chinese Hamster Ovary (CHO) were cells used for protein expression. The cells secreted a mixture of mature TACE beginning with either Val212 or Arg215. TACE-containing fractions from the Ni-NTA column were incubated in a buffer containing octylglucoside and the binding partner N-[D,L-[2-(hydroxyaminocarnbonyl)methyl]-4-methyl-pentanoyl)-L-3-(tert-butyl)-glycyl-L-alanine. The final purification step was performed on a gel filtration column. Purified TACE was stored in a buffer containing 10 mM Tris/HCL pH 7.5, 100 mM NaCl, 10% glycerol and 1 mM of inhibitor (TACE buffer).

Crystallization experiments were set up at a TACE concentration of approximately 5 mg/mL by mixing TACE (in TACE buffer) in a 1:1 ratio with the crystallization buffers listed below and using the sitting drop vapor diffusion technique. The experiments were performed in duplicate and incubated either at about 4°C or at 20°C. Crystalline precipitate was obtained at 20°C in the following crystallization buffers:

Buffer A)	0.1 M Na Acetate pH 5.3, 0.2 M $CaCl_2$, 30% v/v Ethanol
Buffer B)	0.1 M Na Citrate pH 5.0, 40% v/v Ethanol
Buffer C)	0.1 M Na Citrate pH 8.7, 20% w/v PEG 4000, 20% v/v Isopropanol

Small crystals were obtained upon transferring seeds from the crystalline precipitate with a hair of a rabbit into a 1:1 mixture of a concentrated sample of TACE (12 mg/mL in TACE buffer) with either buffer B or C. Further refinement of buffer C resulted in buffer D, which allowed the production of crystals suitable for X-ray data collection.

Buffer D) 0.1 M Na Citrate pH 5.4, 20% w/v PEG 4000, 20% v/v Isopropanol

The first data set was measured to a reduction of 2.5 Å on a MAR300 imaging plate scanner attached to a Rigaku-Denki totaling Cu-anode generator operated at 5.4 kW providing graphite-monochromatized CuKα radiation. The data were processed with MOSFLM v. 5.23 program and routines of the CCP4 suite. All attempts to solve the structure by molecular replacement methods using either adamalysin II, an all-alanine model of adamalysin II and models generated failed to produce useful starting points for phasing. Thus the locations of four independent zinc atoms were determined with the help of an anomalous difference Patterson synthesis. In order to measure MAD data, the crystals were deep-frozen in liquid nitrogen. Therefore, crystals were transferred into a cryo buffer (80% v/v buffer D containing 17% v/v glycerol) with the help of a silk loop of appropriate size, soaked for about 10 seconds and then immediately deep-frozen at 90 degrees K.

The crystals obtained belong to the monoclinic space group $P2_1$, have cell constants a = 61.38 Å (angstrom), b = 126.27 Å, c = 81.27 Å, β = 107.41°, and contain four molecules in the asymmetric unit.

Example 3 - X-ray Diffraction

Using the crystals described in Example 2, a first data set was measured to a resolution of 2.5 Å on a MAR300 imaging plate scanner attached to a Rigaku-Denki rotating Cu-anode generator operated at 5.4kW providing graphite-

monochromatized CuKα radiation. The data were processed at with the MOSFLM v. 5.23 program and routines of the CCP4 suite.

All attempts to solve the structure by molecular replacement methods using either adamalysin II, an all-alanine model of adamalysin II, and other models failed to produce useful starting points for phasing.

Thus, the locations of the four independent zinc atoms were determined with the help of an anomalous difference Patterson synthesis. In order to measure MAD data, the crystals were deep-frozen in a nitrogen gas stream cooled down to the temperature of liquid nitrogen. The crystals were first transferred into a cryo-buffer of 80% v/v Buffer D (0.1 M Na Citrate pH 5.4, 20% w/v PEG 4000, 20% v/v Isopropanol) containing 17% v/v glycerol. Transfer to the cryo-buffer was performed with the help of a silk loop of appropriate size. The crystals were soaked in the cryo-buffer for about 10 seconds and then immediately deep-frozen at 90 K.

Anomalous diffraction data to 2.0 Å were collected with MAR345 imaging plate scanner at 90 K on the BW6 wiggler beamline of DORIS (DESY, Hamburg, Germany), using monochromatic X-ray radiation at the wavelengths of maximal f″ (1.2769 Å) and minimal f′ (1.2776 Å) at the K absorption edge of zinc and at a remote wavelength (1.060 Å). The data were scanned and evaluated using DENZO/SCALEPACK, yielding 77653 independent reflections from 1051836 measurements (96.9% completeness, R-merge 0.031 in intensities).

MAD phases were refined and calculated with MLPHARE including all measured data to 2.0 Å resolution. Their initial mean-figure-of-merit of 0.53 was increased to 0.76 by solvent flattening/histogram matching methods applying DM. This density allowed building of the complete chains of the four independent TACE catalytic domains and the bound hydroxamic acid substrates on an SGI system using TURBO-FRODO. This model was crystallographically refined with XPLOR and with CCP4 routines to a crystallographic R factor of 18.6% (R_{free} 27.4%) using 79400 independent reflections from, 12.0 to 2A. resolution.

Four independent TACE molecules form the periodic arrangement.

Molecules 1 and 2, and 3 and 4 are defined from Asp219 and Met221, respectively, to Ser474.

Example 4 - X-ray Diffraction

Anomalous dispersion diffraction data to 2.0 Å were collected with a MAR345 imaging plate scanner at 100 K on the wiggler beamline of DORIS (DESY, Hamburg, Germany), using monochromatic X-ray radiation of maximal f' (1.2797 Å) and minimal f' (1.2804 Å) at the K absorption edge of zinc and at a remote wavelength (1.060 Å). These data were evaluated and scanned using DENZO/SCALEPACK, yielding 77,653 independent reflections (96.9% completeness, R-merge 0.031).

The structure coordinates obtained are reproduced in Table 1.

TABLE 1

```
REMARK Created by MOLEMAN V. 961218/7.2.5 at Fri Sep 19 20:05:05 1997 for user
carlos
REMARK MoleMan PDB file
CRYST1    61.387  126.278    81.273   90.00    107.42  90.00     P 21          4
ORIGX1       1.000000  0.000000  0.000000        0.00000
ORIGX2       0.000000  1.000000  0.000000        0.00000
ORIGX3       0.000000  0.000000  1.000000        0.00000
SCALE1       0.016290  0.000000  0.005111        0.00000
SCALE2       0.000000  0.007919  0.000000        0.00000
SCALE3       0.000000  0.000000  0.012896        0.00000
```

	Atom	Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1	N	ASP	A	219	0.865	33.077	15.204	1.00	20.00
ATOM	2	OD2	ASP	A	219	5.154	33.868	14.335	1.00	20.00
ATOM	3	OD1	ASP	A	219	4.450	35.924	14.844	1.00	20.00
ATOM	4	CG	ASP	A	219	4.191	34.718	14.461	1.00	20.00
ATOM	5	CB	ASP	A	219	2.738	34.303	14.156	1.00	20.00
ATOM	6	CA	ASP	A	219	2.290	33.026	14.883	1.00	20.00
ATOM	7	C	ASP	A	219	3.166	32.889	16.123	1.00	20.00
ATOM	8	O	ASP	A	219	3.439	33.884	16.819	1.00	20.00
ATOM	9	N	PRO	A	220	3.629	31.679	16.386	1.00	20.00
ATOM	10	CG	PRO	A	220	4.073	29.436	16.118	1.00	20.00
ATOM	11	CD	PRO	A	220	3.224	30.531	15.588	1.00	20.00
ATOM	12	CB	PRO	A	220	4.893	29.974	17.303	1.00	20.00
ATOM	13	CA	PRO	A	220	4.523	31.452	17.495	1.00	20.00
ATOM	14	C	PRO	A	220	5.649	32.530	17.443	1.00	20.00
ATOM	15	O	PRO	A	220	6.513	32.741	18.173	1.00	20.00
ATOM	16	N	MET	A	221	5.766	33.341	16.625	1.00	48.83
ATOM	17	CE	MET	A	221	9.090	36.336	12.584	1.00	53.01
ATOM	18	SD	MET	A	221	9.248	36.147	14.337	1.00	54.21
ATOM	19	CG	MET	A	221	8.515	34.606	14.801	1.00	51.15
ATOM	20	CB	MET	A	221	7.101	34.778	15.298	1.00	48.69
ATOM	21	CA	MET	A	221	6.875	34.306	16.701	1.00	46.22
ATOM	22	C	MET	A	221	6.485	35.500	17.614	1.00	42.51
ATOM	23	O	MET	A	221	7.279	36.002	18.427	1.00	43.93
ATOM	24	N	LYS	A	222	5.215	35.817	17.508	1.00	36.53
ATOM	25	NZ	LYS	A	222	1.844	39.934	13.657	1.00	40.05
ATOM	26	CE	LYS	A	222	2.513	39.901	14.974	1.00	39.09
ATOM	27	CD	LYS	A	222	2.353	38.522	15.613	1.00	38.20
ATOM	28	CG	LYS	A	222	3.646	38.146	16.312	1.00	36.27
ATOM	29	CB	LYS	A	222	3.345	37.404	17.597	1.00	33.97
ATOM	30	CA	LYS	A	222	4.567	36.853	18.299	1.00	32.39
ATOM	31	C	LYS	A	222	4.144	36.220	19.633	1.00	29.13
ATOM	32	O	LYS	A	222	2.999	35.844	19.866	1.00	26.54
ATOM	33	N	ASN	A	223	5.157	36.011	20.462	1.00	23.62
ATOM	34	CA	ASN	A	223	4.951	35.295	21.704	1.00	22.97
ATOM	35	CB	ASN	A	223	5.756	33.987	21.611	1.00	25.44
ATOM	36	CG	ASN	A	223	7.229	34.245	21.372	1.00	26.32
ATOM	37	OD1	ASN	A	223	7.973	33.261	21.243	1.00	29.74
ATOM	38	ND2	ASN	A	223	7.688	35.482	21.319	1.00	25.96
ATOM	39	C	ASN	A	223	5.327	36.123	22.908	1.00	18.46
ATOM	40	O	ASN	A	223	5.365	35.556	23.983	1.00	18.08
ATOM	41	N	THR	A	224	5.611	37.408	22.709	1.00	17.03

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	42	CA	THR	A	224	6.035	38.246	23.824	1.00	16.24
ATOM	43	CB	THR	A	224	7.507	38.721	23.599	1.00	17.52
ATOM	44	OG1	THR	A	224	8.317	37.590	23.318	1.00	16.14
ATOM	45	CG2	THR	A	224	8.002	39.440	24.840	1.00	17.72
ATOM	46	C	THR	A	224	5.152	39.464	24.033	1.00	16.13
ATOM	47	O	THR	A	224	4.863	40.275	23.152	1.00	15.14
ATOM	48	N	CYS	A	225	4.708	39.650	25.253	1.00	16.61
ATOM	49	CA	CYS	A	225	3.915	40.833	25.646	1.00	17.81
ATOM	50	CB	CYS	A	225	2.895	40.460	26.723	1.00	18.01
ATOM	51	SG	CYS	A	225	2.120	41.843	27.562	1.00	18.77
ATOM	52	C	CYS	A	225	4.899	41.914	26.101	1.00	17.46
ATOM	53	O	CYS	A	225	5.614	41.703	27.093	1.00	18.52
ATOM	54	N	LYS	A	226	5.070	42.945	25.285	1.00	17.94
ATOM	55	CA	LYS	A	226	6.011	44.033	25.573	1.00	18.61
ATOM	56	CB	LYS	A	226	6.373	44.816	24.311	1.00	21.04
ATOM	57	CG	LYS	A	226	6.985	43.974	23.202	1.00	22.16
ATOM	58	CD	LYS	A	226	8.395	43.451	23.514	1.00	24.95
ATOM	59	CE	LYS	A	226	8.867	42.585	22.365	1.00	28.75
ATOM	60	NZ	LYS	A	226	10.336	42.445	22.185	1.00	31.31
ATOM	61	C	LYS	A	226	5.461	44.940	26.658	1.00	17.48
ATOM	62	O	LYS	A	226	4.295	45.336	26.642	1.00	16.96
ATOM	63	N	LEU	A	227	6.281	45.274	27.641	1.00	15.78
ATOM	64	CA	LEU	A	227	5.848	46.025	28.777	1.00	15.23
ATOM	65	CB	LEU	A	227	6.182	45.347	30.117	1.00	15.96
ATOM	66	CG	LEU	A	227	5.848	43.884	30.334	1.00	15.88
ATOM	67	CD1	LEU	A	227	6.375	43.381	31.692	1.00	15.72
ATOM	68	CD2	LEU	A	227	4.356	43.646	30.314	1.00	13.61
ATOM	69	C	LEU	A	227	6.462	47.398	28.965	1.00	16.89
ATOM	70	O	LEU	A	227	7.639	47.635	28.725	1.00	17.35
ATOM	71	N	LEU	A	228	5.585	48.248	29.488	1.00	16.01
ATOM	72	CA	LEU	A	228	6.024	49.559	29.935	1.00	15.78
ATOM	73	CB	LEU	A	228	5.105	50.721	29.644	1.00	15.98
ATOM	74	CG	LEU	A	228	5.360	52.012	30.426	1.00	17.60
ATOM	75	CD1	LEU	A	228	6.596	52.712	29.853	1.00	15.81
ATOM	76	CD2	LEU	A	228	4.154	52.945	30.340	1.00	19.40
ATOM	77	C	LEU	A	228	6.144	49.360	31.455	1.00	16.70
ATOM	78	O	LEU	A	228	5.124	49.074	32.104	1.00	16.99
ATOM	79	N	VAL	A	229	7.356	49.488	31.983	1.00	13.83
ATOM	80	CA	VAL	A	229	7.484	49.343	33.450	1.00	12.75
ATOM	81	CB	VAL	A	229	8.600	48.320	33.747	1.00	15.41
ATOM	82	CG1	VAL	A	229	9.015	48.421	35.199	1.00	15.21
ATOM	83	CG2	VAL	A	229	8.062	46.910	33.451	1.00	16.11
ATOM	84	C	VAL	A	229	7.758	50.710	34.055	1.00	11.45
ATOM	85	O	VAL	A	229	8.592	51.462	33.529	1.00	10.78
ATOM	86	N	VAL	A	230	7.029	51.092	35.090	1.00	11.10
ATOM	87	CA	VAL	A	230	7.169	52.397	35.688	1.00	13.35
ATOM	88	CB	VAL	A	230	5.910	53.299	35.518	1.00	13.78
ATOM	89	CG1	VAL	A	230	6.096	54.643	36.192	1.00	13.70
ATOM	90	CG2	VAL	A	230	5.577	53.586	34.050	1.00	12.14
ATOM	91	C	VAL	A	230	7.495	52.252	37.154	1.00	12.98
ATOM	92	O	VAL	A	230	6.791	51.546	37.877	1.00	14.51
ATOM	93	N	ALA	A	231	8.582	52.891	37.570	1.00	14.57
ATOM	94	CA	ALA	A	231	8.915	52.901	39.001	1.00	12.63
ATOM	95	CB	ALA	A	231	10.382	52.556	39.219	1.00	14.54

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	96	C	ALA	A	231	8.616	54.305	39.505	1.00	13.54
ATOM	97	O	ALA	A	231	9.215	55.290	39.004	1.00	12.89
ATOM	98	N	ASP	A	232	7.739	54.412	40.500	1.00	13.89
ATOM	99	CA	ASP	A	232	7.440	55.781	40.947	1.00	15.63
ATOM	100	CB	ASP	A	232	6.061	55.875	41.560	1.00	16.03
ATOM	101	CG	ASP	A	232	5.856	55.198	42.876	1.00	17.24
ATOM	102	OD1	ASP	A	232	4.725	55.249	43.432	1.00	18.20
ATOM	103	OD2	ASP	A	232	6.804	54.565	43.403	1.00	15.69
ATOM	104	C	ASP	A	232	8.559	56.276	41.875	1.00	15.96
ATOM	105	O	ASP	A	232	9.395	55.459	42.253	1.00	13.21
ATOM	106	N	HIS	A	233	8.375	57.492	42.392	1.00	16.98
ATOM	107	CA	HIS	A	233	9.399	58.118	43.244	1.00	16.61
ATOM	108	CB	HIS	A	233	9.075	59.600	43.522	1.00	17.60
ATOM	109	CG	HIS	A	233	7.977	59.866	44.494	1.00	17.74
ATOM	110	CD2	HIS	A	233	8.012	60.040	45.836	1.00	18.92
ATOM	111	ND1	HIS	A	233	6.648	59.946	44.152	1.00	17.72
ATOM	112	CE1	HIS	A	233	5.910	60.144	45.222	1.00	18.19
ATOM	113	NE2	HIS	A	233	6.730	60.214	46.266	1.00	19.56
ATOM	114	C	HIS	A	233	9.562	57.364	44.535	1.00	16.98
ATOM	115	O	HIS	A	233	10.626	57.385	45.170	1.00	14.73
ATOM	116	N	ARG	A	234	8.457	56.762	45.005	1.00	15.26
ATOM	117	CA	ARG	A	234	8.476	55.997	46.231	1.00	16.71
ATOM	118	CB	ARG	A	234	7.083	55.600	46.688	1.00	19.19
ATOM	119	CG	ARG	A	234	6.078	56.729	46.814	1.00	18.94
ATOM	120	CD	ARG	A	234	4.726	56.181	47.250	1.00	21.89
ATOM	121	NE	ARG	A	234	3.696	57.214	47.125	1.00	23.72
ATOM	122	CZ	ARG	A	234	2.872	57.469	48.130	1.00	26.70
ATOM	123	NH1	ARG	A	234	2.923	56.798	49.270	1.00	27.34
ATOM	124	NH2	ARG	A	234	1.953	58.411	47.989	1.00	28.96
ATOM	125	C	ARG	A	234	9.319	54.728	46.062	1.00	17.39
ATOM	126	O	ARG	A	234	10.072	54.359	46.955	1.00	17.02
ATOM	127	N	PHE	A	235	9.149	54.039	44.954	1.00	15.45
ATOM	128	CA	PHE	A	235	9.913	52.829	44.669	1.00	17.15
ATOM	129	CB	PHE	A	235	9.458	52.167	43.370	1.00	15.92
ATOM	130	CG	PHE	A	235	10.063	50.804	43.165	1.00	14.51
ATOM	131	CD1	PHE	A	235	11.226	50.638	42.442	1.00	14.09
ATOM	132	CD2	PHE	A	235	9.429	49.693	43.697	1.00	13.27
ATOM	133	CE1	PHE	A	235	11.786	49.394	42.283	1.00	12.49
ATOM	134	CE2	PHE	A	235	9.979	48.436	43.514	1.00	14.15
ATOM	135	CZ	PHE	A	235	11.159	48.280	42.812	1.00	11.73
ATOM	136	C	PHE	A	235	11.391	53.211	44.502	1.00	15.85
ATOM	137	O	PHE	A	235	12.309	52.611	45.041	1.00	15.02
ATOM	138	N	TYR	A	236	11.573	54.282	43.750	1.00	15.65
ATOM	139	CA	TYR	A	236	12.920	54.781	43.501	1.00	18.77
ATOM	140	CB	TYR	A	236	12.809	56.087	42.744	1.00	20.15
ATOM	141	CG	TYR	A	236	14.079	56.831	42.453	1.00	20.77
ATOM	142	CD1	TYR	A	236	15.006	56.379	41.554	1.00	23.25
ATOM	143	CE1	TYR	A	236	16.171	57.111	41.294	1.00	25.10
ATOM	144	CD2	TYR	A	236	14.303	58.043	43.094	1.00	22.97
ATOM	145	CE2	TYR	A	236	15.434	58.789	42.840	1.00	23.38
ATOM	146	CZ	TYR	A	236	16.355	58.309	41.944	1.00	24.28
ATOM	147	OH	TYR	A	236	17.490	59.032	41.699	1.00	27.10
ATOM	148	C	TYR	A	236	13.668	55.005	44.807	1.00	18.41
ATOM	149	O	TYR	A	236	14.785	54.538	44.979	1.00	17.82

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	150	N	ARG	A	237	13.029	55.671	45.741	1.00	18.84
ATOM	151	NH2	ARG	A	237	16.164	60.578	45.801	1.00	36.66
ATOM	152	NH1	ARG	A	237	15.513	58.642	46.822	1.00	35.42
ATOM	153	CZ	ARG	A	237	15.208	59.704	46.106	1.00	35.99
ATOM	154	NE	ARG	A	237	13.940	59.862	45.712	1.00	36.11
ATOM	155	CD	ARG	A	237	12.867	58.910	45.981	1.00	32.12
ATOM	156	CG	ARG	A	237	12.655	58.442	47.386	1.00	28.99
ATOM	157	CB	ARG	A	237	12.578	56.978	47.698	1.00	22.94
ATOM	158	CA	ARG	A	237	13.566	56.021	47.029	1.00	21.89
ATOM	159	C	ARG	A	237	13.824	54.847	47.959	1.00	22.82
ATOM	160	O	ARG	A	237	14.874	54.759	48.586	1.00	22.33
ATOM	161	N	TYR	A	238	12.826	53.995	48.165	1.00	20.93
ATOM	162	CA	TYR	A	238	12.807	52.950	49.142	1.00	22.79
ATOM	163	CB	TYR	A	238	11.438	52.835	49.835	1.00	25.02
ATOM	164	CG	TYR	A	238	11.052	54.133	50.502	1.00	28.43
ATOM	165	CD1	TYR	A	238	10.191	55.011	49.873	1.00	30.38
ATOM	166	CE1	TYR	A	238	9.827	56.214	50.439	1.00	32.45
ATOM	167	CD2	TYR	A	238	11.570	54.501	51.729	1.00	30.38
ATOM	168	CE2	TYR	A	238	11.228	55.709	52.309	1.00	32.79
ATOM	169	CZ	TYR	A	238	10.384	56.572	51.647	1.00	33.85
ATOM	170	OH	TYR	A	238	10.043	57.784	52.208	1.00	34.86
ATOM	171	C	TYR	A	238	13.222	51.579	48.683	1.00	22.48
ATOM	172	O	TYR	A	238	13.682	50.772	49.509	1.00	24.69
ATOM	173	N	MET	A	239	13.171	51.306	47.405	1.00	20.92
ATOM	174	CA	MET	A	239	13.680	50.048	46.893	1.00	18.57
ATOM	175	CB	MET	A	239	12.667	49.374	45.965	1.00	18.57
ATOM	176	CG	MET	A	239	11.394	48.971	46.729	1.00	18.44
ATOM	177	SD	MET	A	239	11.677	47.664	47.929	1.00	17.64
ATOM	178	CE	MET	A	239	12.084	46.309	46.855	1.00	16.38
ATOM	179	C	MET	A	239	14.975	50.292	46.121	1.00	17.52
ATOM	180	O	MET	A	239	15.826	49.422	46.133	1.00	16.58
ATOM	181	N	GLY	A	240	15.067	51.440	45.447	1.00	16.74
ATOM	182	CA	GLY	A	240	16.198	51.733	44.602	1.00	16.82
ATOM	183	C	GLY	A	240	17.334	52.497	45.232	1.00	20.60
ATOM	184	O	GLY	A	240	18.280	52.875	44.516	1.00	20.21
ATOM	185	N	ARG	A	241	17.242	52.871	46.503	1.00	20.89
ATOM	186	CA	ARG	A	241	18.300	53.628	47.162	1.00	24.17
ATOM	187	CB	ARG	A	241	19.609	52.806	47.126	1.00	26.15
ATOM	188	CG	ARG	A	241	19.504	51.488	47.875	1.00	29.48
ATOM	189	CD	ARG	A	241	20.771	50.648	47.896	1.00	31.73
ATOM	190	NE	ARG	A	241	21.417	50.785	49.228	1.00	32.75
ATOM	191	CZ	ARG	A	241	22.188	51.837	49.428	1.00	33.64
ATOM	192	NH1	ARG	A	241	22.361	52.722	48.450	1.00	35.35
ATOM	193	NH2	ARG	A	241	22.752	52.014	50.598	1.00	32.64
ATOM	194	C	ARG	A	241	18.497	55.001	46.543	1.00	25.05
ATOM	195	O	ARG	A	241	19.574	55.585	46.696	1.00	21.63
ATOM	196	N	GLY	A	242	17.470	55.529	45.831	1.00	22.70
ATOM	197	CA	GLY	A	242	17.603	56.784	45.110	1.00	20.94
ATOM	198	C	GLY	A	242	18.622	56.667	44.003	1.00	20.36
ATOM	199	O	GLY	A	242	19.255	57.656	43.639	1.00	20.42
ATOM	200	N	GLU	A	243	18.841	55.486	43.445	1.00	19.57
ATOM	201	CA	GLU	A	243	19.832	55.277	42.418	1.00	19.51
ATOM	202	CB	GLU	A	243	20.951	54.324	42.832	1.00	21.04
ATOM	203	CG	GLU	A	243	21.992	54.818	43.816	1.00	22.54

	Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	204	CD	GLU	A	243	22.782	53.747	44.543	1.00	24.67
ATOM	205	OE1	GLU	A	243	23.740	54.097	45.292	1.00	24.23
ATOM	206	OE2	GLU	A	243	22.512	52.535	44.451	1.00	22.83
ATOM	207	C	GLU	A	243	19.104	54.717	41.197	1.00	19.62
ATOM	208	O	GLU	A	243	18.414	53.698	41.291	1.00	18.85
ATOM	209	N	GLU	A	244	19.324	55.341	40.075	1.00	19.48
ATOM	210	CA	GLU	A	244	18.699	54.904	38.833	1.00	22.19
ATOM	211	CB	GLU	A	244	18.928	55.950	37.739	1.00	25.49
ATOM	212	CG	GLU	A	244	18.502	55.433	36.371	1.00	29.88
ATOM	213	CD	GLU	A	244	18.409	56.498	35.310	1.00	32.59
ATOM	214	OE1	GLU	A	244	18.205	57.691	35.608	1.00	33.16
ATOM	215	OE2	GLU	A	244	18.528	56.090	34.136	1.00	35.02
ATOM	216	C	GLU	A	244	19.176	53.524	38.414	1.00	21.10
ATOM	217	O	GLU	A	244	18.360	52.654	38.029	1.00	17.68
ATOM	218	N	SER	A	245	20.466	53.247	38.644	1.00	18.06
ATOM	219	CA	SER	A	245	21.001	51.960	38.207	1.00	20.29
ATOM	220	CB	SER	A	245	22.549	51.953	38.270	1.00	21.06
ATOM	221	OG	SER	A	245	22.833	52.394	39.607	1.00	21.74
ATOM	222	C	SER	A	245	20.409	50.844	39.056	1.00	17.46
ATOM	223	O	SER	A	245	19.970	49.834	38.536	1.00	18.81
ATOM	224	N	THR	A	246	20.355	51.020	40.343	1.00	15.88
ATOM	225	CA	THR	A	246	19.821	50.027	41.275	1.00	18.13
ATOM	226	CB	THR	A	246	20.051	50.546	42.689	1.00	19.42
ATOM	227	OG1	THR	A	246	21.459	50.877	42.861	1.00	21.14
ATOM	228	CG2	THR	A	246	19.692	49.547	43.761	1.00	19.86
ATOM	229	C	THR	A	246	18.337	49.757	41.014	1.00	16.92
ATOM	230	O	THR	A	246	17.915	48.619	41.068	1.00	14.90
ATOM	231	N	THR	A	247	17.545	50.799	40.800	1.00	17.19
ATOM	232	CA	THR	A	247	16.108	50.689	40.560	1.00	16.84
ATOM	233	CB	THR	A	247	15.458	52.076	40.443	1.00	16.21
ATOM	234	OG1	THR	A	247	15.860	52.839	41.581	1.00	14.61
ATOM	235	CG2	THR	A	247	13.920	52.069	40.449	1.00	14.87
ATOM	236	C	THR	A	247	15.848	49.892	39.308	1.00	15.69
ATOM	237	O	THR	A	247	15.088	48.922	39.295	1.00	14.94
ATOM	238	N	THR	A	248	16.502	50.305	38.232	1.00	16.92
ATOM	239	CA	THR	A	248	16.382	49.685	36.926	1.00	16.92
ATOM	240	CB	THR	A	248	17.322	50.415	35.963	1.00	17.93
ATOM	241	OG1	THR	A	248	16.875	51.787	35.915	1.00	18.06
ATOM	242	CG2	THR	A	248	17.381	49.792	34.586	1.00	19.15
ATOM	243	C	THR	A	248	16.712	48.202	36.972	1.00	18.22
ATOM	244	O	THR	A	248	16.073	47.313	36.427	1.00	14.91
ATOM	245	N	ASN	A	249	17.857	47.907	37.593	1.00	17.46
ATOM	246	CA	ASN	A	249	18.342	46.545	37.700	1.00	17.81
ATOM	247	CB	ASN	A	249	19.723	46.472	38.349	1.00	19.11
ATOM	248	CG	ASN	A	249	20.854	47.016	37.499	1.00	22.53
ATOM	249	OD1	ASN	A	249	20.753	47.173	36.283	1.00	22.82
ATOM	250	ND2	ASN	A	249	21.989	47.306	38.157	1.00	21.73
ATOM	251	C	ASN	A	249	17.364	45.662	38.478	1.00	15.16
ATOM	252	O	ASN	A	249	17.157	44.510	38.066	1.00	13.94
ATOM	253	N	TYR	A	250	16.850	46.170	39.578	1.00	14.10
ATOM	254	CA	TYR	A	250	15.888	45.426	40.360	1.00	15.67
ATOM	255	CB	TYR	A	250	15.393	46.239	41.546	1.00	16.52
ATOM	256	CG	TYR	A	250	14.527	45.444	42.501	1.00	19.76
ATOM	257	CD1	TYR	A	250	15.109	44.778	43.571	1.00	20.38

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	258	CE1	TYR	A	250	14.344	44.031	44.447	1.00	21.56
ATOM	259	CD2	TYR	A	250	13.138	45.344	42.332	1.00	18.76
ATOM	260	CE2	TYR	A	250	12.377	44.600	43.203	1.00	19.63
ATOM	261	CZ	TYR	A	250	12.985	43.943	44.248	1.00	22.22
ATOM	262	OH	TYR	A	250	12.250	43.189	45.134	1.00	24.91
ATOM	263	C	TYR	A	250	14.683	45.029	39.472	1.00	14.95
ATOM	264	O	TYR	A	250	14.234	43.893	39.546	1.00	11.83
ATOM	265	N	LEU	A	251	14.133	46.021	38.758	1.00	13.07
ATOM	266	CA	LEU	A	251	12.977	45.742	37.899	1.00	12.72
ATOM	267	CB	LEU	A	251	12.271	47.059	37.519	1.00	12.66
ATOM	268	CG	LEU	A	251	11.696	47.800	38.734	1.00	14.96
ATOM	269	CD1	LEU	A	251	11.038	49.099	38.363	1.00	18.53
ATOM	270	CD2	LEU	A	251	10.717	46.914	39.501	1.00	19.00
ATOM	271	C	LEU	A	251	13.288	44.885	36.700	1.00	11.35
ATOM	272	O	LEU	A	251	12.518	43.962	36.349	1.00	10.33
ATOM	273	N	ILE	A	252	14.429	45.093	36.050	1.00	10.29
ATOM	274	CA	ILE	A	252	14.832	44.209	34.944	1.00	12.09
ATOM	275	CB	ILE	A	252	16.209	44.654	34.372	1.00	13.58
ATOM	276	CG2	ILE	A	252	16.848	43.570	33.523	1.00	14.17
ATOM	277	CG1	ILE	A	252	16.059	45.964	33.581	1.00	16.57
ATOM	278	CD1	ILE	A	252	17.351	46.450	32.902	1.00	18.53
ATOM	279	C	ILE	A	252	14.938	42.791	35.448	1.00	10.51
ATOM	280	O	ILE	A	252	14.592	41.830	34.755	1.00	12.14
ATOM	281	N	GLU	A	253	15.508	42.598	36.641	1.00	9.27
ATOM	282	CA	GLU	A	253	15.743	41.263	37.159	1.00	10.71
ATOM	283	CB	GLU	A	253	16.762	41.233	38.306	1.00	12.25
ATOM	284	CG	GLU	A	253	18.217	41.412	37.830	1.00	12.76
ATOM	285	CD	GLU	A	253	19.215	41.029	38.924	1.00	15.62
ATOM	286	OE1	GLU	A	253	19.091	40.009	39.615	1.00	14.92
ATOM	287	OE2	GLU	A	253	20.134	41.798	39.207	1.00	14.69
ATOM	288	C	GLU	A	253	14.422	40.619	37.605	1.00	9.88
ATOM	289	O	GLU	A	253	14.195	39.441	37.388	1.00	7.43
ATOM	290	N	LEU	A	254	13.559	41.420	38.230	1.00	10.47
ATOM	291	CA	LEU	A	254	12.266	40.858	38.649	1.00	10.04
ATOM	292	CB	LEU	A	254	11.537	41.807	39.572	1.00	9.92
ATOM	293	CG	LEU	A	254	10.103	41.493	40.022	1.00	10.99
ATOM	294	CD1	LEU	A	254	9.778	42.322	41.239	1.00	11.71
ATOM	295	CD2	LEU	A	254	9.106	41.854	38.918	1.00	11.46
ATOM	296	C	LEU	A	254	11.481	40.463	37.408	1.00	9.41
ATOM	297	O	LEU	A	254	10.959	39.343	37.426	1.00	10.16
ATOM	298	N	ILE	A	255	11.399	41.269	36.369	1.00	11.15
ATOM	299	CA	ILE	A	255	10.590	40.910	35.180	1.00	11.06
ATOM	300	CB	ILE	A	255	10.480	42.108	34.194	1.00	10.34
ATOM	301	CG2	ILE	A	255	9.910	41.651	32.851	1.00	12.31
ATOM	302	CG1	ILE	A	255	9.646	43.216	34.796	1.00	10.06
ATOM	303	CD1	ILE	A	255	8.235	42.810	35.286	1.00	10.90
ATOM	304	C	ILE	A	255	11.113	39.671	34.495	1.00	11.34
ATOM	305	O	ILE	A	255	10.466	38.704	34.055	1.00	8.95
ATOM	306	N	ASP	A	256	12.458	39.596	34.420	1.00	10.09
ATOM	307	CA	ASP	A	256	13.108	38.362	33.953	1.00	11.00
ATOM	308	CB	ASP	A	256	14.621	38.617	33.890	1.00	12.60
ATOM	309	CG	ASP	A	256	15.320	37.358	33.434	1.00	16.54
ATOM	310	OD1	ASP	A	256	15.159	37.033	32.249	1.00	17.04
ATOM	311	OD2	ASP	A	256	15.977	36.731	34.290	1.00	18.15

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	312	C	ASP	A	256	12.763	37.124	34.779	1.00	10.53
ATOM	313	O	ASP	A	256	12.485	36.036	34.246	1.00	11.14
ATOM	314	N	ARG	A	257	12.719	37.177	36.087	1.00	11.51
ATOM	315	CA	ARG	A	257	12.362	36.025	36.923	1.00	11.03
ATOM	316	CB	ARG	A	257	12.646	36.291	38.375	1.00	11.04
ATOM	317	CG	ARG	A	257	14.194	36.302	38.743	1.00	9.97
ATOM	318	CD	ARG	A	257	14.347	36.333	40.258	1.00	9.94
ATOM	319	NE	ARG	A	257	13.581	37.392	40.951	1.00	9.56
ATOM	320	CZ	ARG	A	257	14.058	38.613	41.124	1.00	10.48
ATOM	321	NH1	ARG	A	257	15.283	38.961	40.677	1.00	8.64
ATOM	322	NH2	ARG	A	257	13.363	39.539	41.718	1.00	8.45
ATOM	323	C	ARG	A	257	10.868	35.673	36.655	1.00	10.99
ATOM	324	O	ARG	A	257	10.495	34.509	36.580	1.00	10.38
ATOM	325	N	VAL	A	258	10.033	36.685	36.635	1.00	7.90
ATOM	326	CA	VAL	A	258	8.600	36.497	36.295	1.00	9.48
ATOM	327	CB	VAL	A	258	7.877	37.856	36.335	1.00	8.97
ATOM	328	CG1	VAL	A	258	6.398	37.717	35.905	1.00	7.38
ATOM	329	CG2	VAL	A	258	7.915	38.447	37.733	1.00	7.76
ATOM	330	C	VAL	A	258	8.469	35.851	34.931	1.00	9.20
ATOM	331	O	VAL	A	258	7.769	34.858	34.706	1.00	11.73
ATOM	332	N	ASP	A	259	9.193	36.330	33.947	1.00	10.44
ATOM	333	CA	ASP	A	259	9.196	35.817	32.585	1.00	11.92
ATOM	334	CB	ASP	A	259	10.101	36.614	31.655	1.00	12.64
ATOM	335	CG	ASP	A	259	10.059	36.157	30.219	1.00	17.49
ATOM	336	OD1	ASP	A	259	8.962	36.007	29.644	1.00	16.26
ATOM	337	OD2	ASP	A	259	11.145	35.932	29.637	1.00	20.54
ATOM	338	C	ASP	A	259	9.618	34.346	32.546	1.00	13.21
ATOM	339	O	ASP	A	259	9.021	33.572	31.783	1.00	11.13
ATOM	340	N	ASP	A	260	10.546	33.904	33.412	1.00	12.46
ATOM	341	OD2	ASP	A	260	14.081	33.042	35.067	1.00	19.42
ATOM	342	OD1	ASP	A	260	13.629	33.074	32.936	1.00	15.68
ATOM	343	CG	ASP	A	260	13.335	32.789	34.098	1.00	16.09
ATOM	344	CB	ASP	A	260	11.972	32.171	34.451	1.00	13.52
ATOM	345	CA	ASP	A	260	10.912	32.498	33.403	1.00	11.20
ATOM	346	C	ASP	A	260	9.647	31.669	33.761	1.00	13.45
ATOM	347	O	ASP	A	260	9.461	30.565	33.241	1.00	11.34
ATOM	348	N	ILE	A	261	8.867	32.202	34.720	1.00	10.81
ATOM	349	CA	ILE	A	261	7.643	31.469	35.052	1.00	11.86
ATOM	350	CB	ILE	A	261	6.910	32.167	36.198	1.00	13.06
ATOM	351	CG2	ILE	A	261	5.538	31.612	36.416	1.00	12.50
ATOM	352	CG1	ILE	A	261	7.825	31.986	37.422	1.00	16.02
ATOM	353	CD1	ILE	A	261	7.242	32.547	38.701	1.00	17.40
ATOM	354	C	ILE	A	261	6.738	31.396	33.815	1.00	10.07
ATOM	355	O	ILE	A	261	6.351	30.273	33.480	1.00	11.72
ATOM	356	N	TYR	A	262	6.434	32.522	33.232	1.00	8.70
ATOM	357	CA	TYR	A	262	5.515	32.515	32.082	1.00	11.55
ATOM	358	CB	TYR	A	262	5.275	33.937	31.548	1.00	11.91
ATOM	359	CG	TYR	A	262	4.257	34.650	32.411	1.00	12.15
ATOM	360	CD1	TYR	A	262	4.554	35.110	33.670	1.00	12.29
ATOM	361	CE1	TYR	A	262	3.598	35.746	34.457	1.00	12.53
ATOM	362	CD2	TYR	A	262	2.940	34.799	31.941	1.00	14.52
ATOM	363	CE2	TYR	A	262	1.989	35.420	32.716	1.00	14.04
ATOM	364	CZ	TYR	A	262	2.315	35.905	33.956	1.00	14.14
ATOM	365	OH	TYR	A	262	1.368	36.538	34.724	1.00	12.39

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	366	C	TYR	A	262	5.982	31.682	30.932	1.00	11.66
ATOM	367	O	TYR	A	262	5.202	30.842	30.446	1.00	11.39
ATOM	368	N	ARG	A	263	7.231	31.887	30.478	1.00	10.78
ATOM	369	CA	ARG	A	263	7.771	31.180	29.333	1.00	14.61
ATOM	370	CB	ARG	A	263	9.236	31.623	29.117	1.00	18.66
ATOM	371	CG	ARG	A	263	9.634	32.729	28.194	1.00	21.81
ATOM	372	CD	ARG	A	263	11.103	32.655	27.718	1.00	25.82
ATOM	373	NE	ARG	A	263	11.932	31.745	28.516	1.00	27.30
ATOM	374	CZ	ARG	A	263	12.427	32.092	29.708	1.00	28.71
ATOM	375	NH1	ARG	A	263	12.225	33.329	30.166	1.00	29.09
ATOM	376	NH2	ARG	A	263	13.087	31.212	30.435	1.00	27.05
ATOM	377	C	ARG	A	263	7.751	29.674	29.425	1.00	15.13
ATOM	378	O	ARG	A	263	7.596	28.973	28.384	1.00	17.45
ATOM	379	N	ASN	A	264	8.019	29.078	30.591	1.00	12.82
ATOM	380	CA	ASN	A	264	8.003	27.677	30.834	1.00	14.56
ATOM	381	CB	ASN	A	264	8.878	27.204	32.013	1.00	17.95
ATOM	382	CG	ASN	A	264	10.323	27.555	31.654	1.00	19.62
ATOM	383	OD1	ASN	A	264	10.776	27.002	30.654	1.00	23.25
ATOM	384	ND2	ASN	A	264	10.957	28.464	32.335	1.00	19.81
ATOM	385	C	ASN	A	264	6.582	27.144	31.076	1.00	16.00
ATOM	386	O	ASN	A	264	6.449	25.944	31.293	1.00	14.82
ATOM	387	N	THR	A	265	5.566	28.017	31.073	1.00	13.74
ATOM	388	CA	THR	A	265	4.221	27.425	31.290	1.00	13.37
ATOM	389	CB	THR	A	265	3.309	28.463	31.935	1.00	14.37
ATOM	390	OG1	THR	A	265	3.800	28.787	33.238	1.00	11.71
ATOM	391	CG2	THR	A	265	1.866	27.953	32.101	1.00	12.84
ATOM	392	C	THR	A	265	3.675	26.917	29.965	1.00	12.82
ATOM	393	O	THR	A	265	3.698	27.628	28.968	1.00	14.37
ATOM	394	N	ALA	A	266	3.134	25.708	29.970	1.00	13.65
ATOM	395	CA	ALA	A	266	2.432	25.151	28.820	1.00	14.19
ATOM	396	CB	ALA	A	266	2.737	23.645	28.812	1.00	14.17
ATOM	397	C	ALA	A	266	0.937	25.431	28.997	1.00	11.04
ATOM	398	O	ALA	A	266	0.250	24.682	29.675	1.00	10.22
ATOM	399	N	TRP	A	267	0.426	26.539	28.524	1.00	11.35
ATOM	400	CA	TRP	A	267	-0.962	26.949	28.736	1.00	13.04
ATOM	401	CB	TRP	A	267	-1.183	28.301	28.045	1.00	11.63
ATOM	402	CG	TRP	A	267	-0.186	29.330	28.523	1.00	10.70
ATOM	403	CD2	TRP	A	267	-0.205	29.920	29.819	1.00	8.77
ATOM	404	CE2	TRP	A	267	0.904	30.814	29.863	1.00	12.19
ATOM	405	CE3	TRP	A	267	-1.007	29.828	30.931	1.00	9.72
ATOM	406	CD1	TRP	A	267	0.865	29.846	27.849	1.00	10.38
ATOM	407	NE1	TRP	A	267	1.531	30.754	28.652	1.00	11.35
ATOM	408	CZ2	TRP	A	267	1.187	31.580	30.989	1.00	10.57
ATOM	409	CZ3	TRP	A	267	-0.718	30.580	32.066	1.00	11.82
ATOM	410	CH2	TRP	A	267	0.395	31.439	32.071	1.00	9.78
ATOM	411	C	TRP	A	267	-2.007	25.919	28.298	1.00	14.01
ATOM	412	O	TRP	A	267	-3.089	25.832	28.915	1.00	14.19
ATOM	413	N	ASP	A	268	-1.688	25.091	27.326	1.00	11.86
ATOM	414	CA	ASP	A	268	-2.615	24.026	26.899	1.00	13.82
ATOM	415	CB	ASP	A	268	-2.765	24.051	25.382	1.00	13.92
ATOM	416	CG	ASP	A	268	-1.517	23.691	24.619	1.00	16.74
ATOM	417	OD1	ASP	A	268	-0.422	23.699	25.244	1.00	16.49
ATOM	418	OD2	ASP	A	268	-1.561	23.395	23.404	1.00	15.38
ATOM	419	C	ASP	A	268	-2.165	22.661	27.367	1.00	15.26

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	420	O	ASP	A	268	-2.554	21.608	26.834	1.00	13.18
ATOM	421	N	ASN	A	269	-1.225	22.609	28.329	1.00	14.90
ATOM	422	CA	ASN	A	269	-0.596	21.391	28.792	1.00	15.45
ATOM	423	CB	ASN	A	269	-1.547	20.454	29.549	1.00	17.28
ATOM	424	CG	ASN	A	269	-2.190	21.182	30.719	1.00	18.96
ATOM	425	OD1	ASN	A	269	-1.464	21.670	31.560	1.00	20.34
ATOM	426	ND2	ASN	A	269	-3.500	21.321	30.788	1.00	18.93
ATOM	427	C	ASN	A	269	0.108	20.556	27.711	1.00	14.79
ATOM	428	O	ASN	A	269	0.330	19.352	27.859	1.00	14.35
ATOM	429	N	ALA	A	270	0.523	21.193	26.654	1.00	14.55
ATOM	430	CA	ALA	A	270	1.203	20.593	25.533	1.00	17.42
ATOM	431	CB	ALA	A	270	0.189	20.155	24.481	1.00	15.76
ATOM	432	C	ALA	A	270	2.239	21.573	25.004	1.00	16.67
ATOM	433	O	ALA	A	270	3.183	21.866	25.757	1.00	19.13
ATOM	434	N	GLY	A	271	2.143	22.004	23.765	1.00	16.01
ATOM	435	CA	GLY	A	271	3.174	22.837	23.177	1.00	18.64
ATOM	436	C	GLY	A	271	2.951	24.321	23.125	1.00	17.56
ATOM	437	O	GLY	A	271	3.768	25.075	22.589	1.00	18.20
ATOM	438	N	PHE	A	272	1.844	24.831	23.659	1.00	17.81
ATOM	439	CA	PHE	A	272	1.538	26.263	23.614	1.00	16.42
ATOM	440	CB	PHE	A	272	0.047	26.539	23.710	1.00	16.73
ATOM	441	CG	PHE	A	272	-0.389	27.890	23.205	1.00	17.94
ATOM	442	CD1	PHE	A	272	-0.462	28.168	21.858	1.00	19.17
ATOM	443	CD2	PHE	A	272	-0.716	28.894	24.100	1.00	18.80
ATOM	444	CE1	PHE	A	272	-0.813	29.421	21.407	1.00	18.87
ATOM	445	CE2	PHE	A	272	-1.120	30.139	23.664	1.00	18.81
ATOM	446	CZ	PHE	A	272	-1.142	30.404	22.310	1.00	19.11
ATOM	447	C	PHE	A	272	2.305	26.889	24.796	1.00	16.83
ATOM	448	O	PHE	A	272	1.786	27.138	25.860	1.00	14.19
ATOM	449	N	LYS	A	273	3.584	27.067	24.561	1.00	17.93
ATOM	450	CA	LYS	A	273	4.522	27.543	25.546	1.00	21.35
ATOM	451	CB	LYS	A	273	5.236	26.296	26.080	1.00	24.32
ATOM	452	CG	LYS	A	273	6.157	25.698	25.023	1.00	27.94
ATOM	453	CD	LYS	A	273	6.625	24.300	25.389	1.00	31.29
ATOM	454	CE	LYS	A	273	7.307	24.300	26.732	1.00	32.80
ATOM	455	NZ	LYS	A	273	6.347	24.136	27.857	1.00	33.38
ATOM	456	C	LYS	A	273	5.479	28.518	24.906	1.00	19.96
ATOM	457	O	LYS	A	273	5.444	28.763	23.706	1.00	18.61
ATOM	458	N	GLY	A	274	6.382	29.094	25.709	1.00	20.59
ATOM	459	CA	GLY	A	274	7.323	30.058	25.166	1.00	17.10
ATOM	460	C	GLY	A	274	6.701	31.449	25.153	1.00	17.80
ATOM	461	O	GLY	A	274	7.272	32.334	24.547	1.00	17.48
ATOM	462	N	TYR	A	275	5.527	31.675	25.763	1.00	15.67
ATOM	463	CA	TYR	A	275	4.892	32.965	25.802	1.00	16.24
ATOM	464	CB	TYR	A	275	3.340	32.874	25.854	1.00	15.81
ATOM	465	CG	TYR	A	275	2.838	32.446	24.503	1.00	17.73
ATOM	466	CD1	TYR	A	275	2.784	31.102	24.175	1.00	17.51
ATOM	467	CE1	TYR	A	275	2.384	30.722	22.919	1.00	20.42
ATOM	468	CD2	TYR	A	275	2.524	33.418	23.543	1.00	18.48
ATOM	469	CE2	TYR	A	275	2.140	33.017	22.279	1.00	20.02
ATOM	470	CZ	TYR	A	275	2.065	31.690	21.989	1.00	19.42
ATOM	471	OH	TYR	A	275	1.670	31.304	20.737	1.00	23.70
ATOM	472	C	TYR	A	275	5.317	33.689	27.087	1.00	15.60
ATOM	473	O	TYR	A	275	5.270	33.077	28.160	1.00	15.87

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	474	N	GLY	A	276	5.638	34.959	26.991	1.00	17.04
ATOM	475	CA	GLY	A	276	5.978	35.692	28.190	1.00	17.48
ATOM	476	C	GLY	A	276	5.988	37.183	28.020	1.00	19.17
ATOM	477	O	GLY	A	276	5.226	37.781	27.278	1.00	16.76
ATOM	478	N	ILE	A	277	6.893	37.805	28.811	1.00	18.66
ATOM	479	CA	ILE	A	277	6.938	39.245	28.907	1.00	17.89
ATOM	480	CB	ILE	A	277	6.413	39.745	30.256	1.00	19.63
ATOM	481	CG2	ILE	A	277	4.925	39.409	30.421	1.00	21.02
ATOM	482	CG1	ILE	A	277	7.212	39.101	31.390	1.00	20.19
ATOM	483	CD1	ILE	A	277	6.754	39.439	32.779	1.00	20.94
ATOM	484	C	ILE	A	277	8.385	39.741	28.763	1.00	18.46
ATOM	485	O	ILE	A	277	9.318	39.076	29.168	1.00	16.61
ATOM	486	N	GLN	A	278	8.505	40.919	28.219	1.00	17.96
ATOM	487	CA	GLN	A	278	9.743	41.629	28.051	1.00	19.65
ATOM	488	CB	GLN	A	278	10.224	41.684	26.624	1.00	25.01
ATOM	489	CG	GLN	A	278	11.692	41.405	26.382	1.00	28.24
ATOM	490	CD	GLN	A	278	11.580	40.059	25.643	1.00	32.63
ATOM	491	OE1	GLN	A	278	11.660	40.060	24.422	1.00	33.32
ATOM	492	NE2	GLN	A	278	11.331	39.078	26.502	1.00	34.14
ATOM	493	C	GLN	A	278	9.499	43.122	28.316	1.00	17.44
ATOM	494	O	GLN	A	278	8.589	43.689	27.693	1.00	14.22
ATOM	495	N	ILE	A	279	10.537	43.709	28.900	1.00	13.53
ATOM	496	CA	ILE	A	279	10.471	45.146	29.090	1.00	15.82
ATOM	497	CB	ILE	A	279	11.441	45.658	30.183	1.00	15.54
ATOM	498	CG2	ILE	A	279	11.402	47.166	30.140	1.00	15.97
ATOM	499	CG1	ILE	A	279	11.007	45.083	31.520	1.00	16.27
ATOM	500	CD1	ILE	A	279	11.940	45.388	32.661	1.00	17.52
ATOM	501	C	ILE	A	279	10.745	45.847	27.771	1.00	16.97
ATOM	502	O	ILE	A	279	11.741	45.578	27.115	1.00	16.40
ATOM	503	N	GLU	A	280	9.824	46.719	27.370	1.00	17.63
ATOM	504	CA	GLU	A	280	10.019	47.523	26.185	1.00	20.86
ATOM	505	CB	GLU	A	280	8.744	47.778	25.395	1.00	23.07
ATOM	506	CG	GLU	A	280	8.890	48.784	24.268	1.00	29.11
ATOM	507	CD	GLU	A	280	9.843	48.327	23.189	1.00	32.61
ATOM	508	OE1	GLU	A	280	10.187	47.124	23.154	1.00	36.14
ATOM	509	OE2	GLU	A	280	10.293	49.127	22.343	1.00	34.84
ATOM	510	C	GLU	A	280	10.599	48.892	26.605	1.00	18.21
ATOM	511	O	GLU	A	280	11.426	49.511	25.941	1.00	16.53
ATOM	512	N	GLN	A	281	10.088	49.380	27.716	1.00	18.36
ATOM	513	NE2	GLN	A	281	11.497	53.112	26.056	1.00	34.24
ATOM	514	OE1	GLN	A	281	10.702	55.093	26.755	1.00	36.11
ATOM	515	CD	GLN	A	281	10.798	53.869	26.901	1.00	33.14
ATOM	516	CG	GLN	A	281	10.120	53.163	28.056	1.00	29.67
ATOM	517	CB	GLN	A	281	9.611	51.793	27.640	1.00	24.17
ATOM	518	CA	GLN	A	281	10.509	50.675	28.207	1.00	21.85
ATOM	519	C	GLN	A	281	10.385	50.730	29.723	1.00	22.08
ATOM	520	O	GLN	A	281	9.444	50.170	30.275	1.00	19.43
ATOM	521	N	ILE	A	282	11.379	51.377	30.337	1.00	19.26
ATOM	522	CA	ILE	A	282	11.340	51.564	31.756	1.00	20.21
ATOM	523	CB	ILE	A	282	12.456	50.838	32.501	1.00	23.17
ATOM	524	CG2	ILE	A	282	12.567	51.331	33.942	1.00	22.63
ATOM	525	CG1	ILE	A	282	12.183	49.337	32.486	1.00	24.53
ATOM	526	CD1	ILE	A	282	13.292	48.530	33.126	1.00	27.43
ATOM	527	C	ILE	A	282	11.408	53.062	32.033	1.00	20.13

	Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	528	O	ILE	A	282	12.183	53.826	31.441	1.00	21.53
ATOM	529	N	ARG	A	283	10.595	53.478	32.972	1.00	18.99
ATOM	530	CA	ARG	A	283	10.541	54.878	33.353	1.00	20.71
ATOM	531	CB	ARG	A	283	9.159	55.499	33.116	1.00	23.74
ATOM	532	CG	ARG	A	283	8.779	55.516	31.645	1.00	28.61
ATOM	533	CD	ARG	A	283	9.030	56.887	31.041	1.00	33.16
ATOM	534	NE	ARG	A	283	9.596	56.759	29.712	1.00	37.40
ATOM	535	CZ	ARG	A	283	9.199	57.449	28.659	1.00	40.44
ATOM	536	NH1	ARG	A	283	8.191	58.311	28.783	1.00	41.71
ATOM	537	NH2	ARG	A	283	9.800	57.245	27.492	1.00	41.03
ATOM	538	C	ARG	A	283	10.826	54.930	34.844	1.00	20.40
ATOM	539	O	ARG	A	283	10.049	54.339	35.566	1.00	17.37
ATOM	540	N	ILE	A	284	11.881	55.634	35.220	1.00	18.94
ATOM	541	CA	ILE	A	284	12.127	55.779	36.655	1.00	19.58
ATOM	542	CB	ILE	A	284	13.582	55.519	37.053	1.00	20.09
ATOM	543	CG2	ILE	A	284	13.684	55.477	38.573	1.00	20.97
ATOM	544	CG1	ILE	A	284	14.178	54.254	36.460	1.00	20.86
ATOM	545	CD1	ILE	A	284	13.442	52.976	36.774	1.00	20.01
ATOM	546	C	ILE	A	284	11.792	57.228	37.002	1.00	19.71
ATOM	547	O	ILE	A	284	12.399	58.147	36.427	1.00	19.08
ATOM	548	N	LEU	A	285	10.816	57.413	37.849	1.00	19.33
ATOM	549	CA	LEU	A	285	10.379	58.729	38.276	1.00	20.90
ATOM	550	CB	LEU	A	285	8.881	58.729	38.557	1.00	20.57
ATOM	551	CG	LEU	A	285	8.020	58.220	37.391	1.00	18.92
ATOM	552	CD1	LEU	A	285	6.569	58.488	37.719	1.00	19.77
ATOM	553	CD2	LEU	A	285	8.426	58.759	36.039	1.00	18.79
ATOM	554	C	LEU	A	285	11.153	59.078	39.542	1.00	22.65
ATOM	555	O	LEU	A	285	10.861	58.536	40.585	1.00	21.09
ATOM	556	N	LYS	A	286	12.179	59.897	39.370	1.00	23.47
ATOM	557	CA	LYS	A	286	13.101	60.223	40.443	1.00	25.88
ATOM	558	CB	LYS	A	286	14.400	60.777	39.830	1.00	24.64
ATOM	559	CG	LYS	A	286	15.057	59.703	38.969	1.00	26.69
ATOM	560	CD	LYS	A	286	16.105	60.262	38.032	1.00	28.58
ATOM	561	CE	LYS	A	286	17.308	59.334	37.986	1.00	28.89
ATOM	562	NZ	LYS	A	286	18.328	59.807	37.012	1.00	29.92
ATOM	563	C	LYS	A	286	12.515	61.157	41.473	1.00	26.73
ATOM	564	O	LYS	A	286	12.944	61.136	42.622	1.00	28.60
ATOM	565	N	SER	A	287	11.543	61.980	41.133	1.00	25.80
ATOM	566	CA	SER	A	287	10.969	62.865	42.158	1.00	26.18
ATOM	567	CB	SER	A	287	11.627	64.249	42.056	1.00	26.60
ATOM	568	OG	SER	A	287	11.272	64.767	40.796	1.00	28.18
ATOM	569	C	SER	A	287	9.471	62.857	41.977	1.00	24.89
ATOM	570	O	SER	A	287	8.996	62.358	40.947	1.00	25.47
ATOM	571	N	PRO	A	288	8.739	63.268	42.989	1.00	26.04
ATOM	572	CD	PRO	A	288	9.222	63.876	44.247	1.00	27.14
ATOM	573	CA	PRO	A	288	7.294	63.276	42.938	1.00	26.70
ATOM	574	CB	PRO	A	288	6.831	63.561	44.339	1.00	26.05
ATOM	575	CG	PRO	A	288	8.010	63.972	45.128	1.00	27.69
ATOM	576	C	PRO	A	288	6.826	64.313	41.928	1.00	27.00
ATOM	577	O	PRO	A	288	7.522	65.301	41.666	1.00	27.28
ATOM	578	N	GLN	A	289	5.681	64.051	41.341	1.00	25.80
ATOM	579	CA	GLN	A	289	5.123	64.976	40.376	1.00	27.15
ATOM	580	CB	GLN	A	289	4.021	64.214	39.628	1.00	27.78
ATOM	581	CG	GLN	A	289	3.246	65.040	38.617	1.00	27.92

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	582	CD	GLN	A	289	4.207	65.636	37.616	1.00	28.41
ATOM	583	OE1	GLN	A	289	4.970	64.944	36.966	1.00	28.03
ATOM	584	NE2	GLN	A	289	4.179	66.966	37.505	1.00	32.04
ATOM	585	C	GLN	A	289	4.553	66.194	41.093	1.00	27.84
ATOM	586	O	GLN	A	289	3.693	66.017	41.943	1.00	27.12
ATOM	587	N	GLU	A	290	4.962	67.414	40.766	1.00	30.72
ATOM	588	OE2	GLU	A	290	4.477	72.113	38.486	1.00	39.70
ATOM	589	OE1	GLU	A	290	6.067	72.564	39.857	1.00	40.48
ATOM	590	CD	GLU	A	290	5.336	71.724	39.305	1.00	39.53
ATOM	591	CG	GLU	A	290	5.461	70.253	39.660	1.00	37.94
ATOM	592	CB	GLU	A	290	5.094	69.910	41.084	1.00	35.71
ATOM	593	CA	GLU	A	290	4.384	68.595	41.401	1.00	33.44
ATOM	594	C	GLU	A	290	2.912	68.679	40.978	1.00	32.66
ATOM	595	O	GLU	A	290	2.615	68.487	39.807	1.00	32.60
ATOM	596	N	VAL	A	291	2.027	68.929	41.928	1.00	32.52
ATOM	597	CA	VAL	A	291	0.589	68.960	41.608	1.00	34.53
ATOM	598	CB	VAL	A	291	0.016	67.667	42.214	1.00	34.68
ATOM	599	CG1	VAL	A	291	-0.992	67.828	43.317	1.00	33.99
ATOM	600	CG2	VAL	A	291	-0.509	66.742	41.114	1.00	33.97
ATOM	601	C	VAL	A	291	-0.040	70.265	42.070	1.00	36.93
ATOM	602	O	VAL	A	291	0.296	70.786	43.141	1.00	35.77
ATOM	603	N	LYS	A	292	-0.879	70.860	41.231	1.00	38.91
ATOM	604	NZ	LYS	A	292	0.250	74.239	36.361	1.00	47.09
ATOM	605	CE	LYS	A	292	-0.459	74.753	37.563	1.00	45.89
ATOM	606	CD	LYS	A	292	-1.298	73.665	38.215	1.00	45.49
ATOM	607	CG	LYS	A	292	-1.226	73.759	39.722	1.00	44.08
ATOM	608	CB	LYS	A	292	-2.197	72.809	40.397	1.00	42.31
ATOM	609	CA	LYS	A	292	-1.595	72.078	41.589	1.00	41.28
ATOM	610	C	LYS	A	292	-2.701	71.697	42.557	1.00	41.79
ATOM	611	O	LYS	A	292	-3.085	70.535	42.624	1.00	42.72
ATOM	612	N	PRO	A	293	-3.192	72.668	43.305	1.00	42.21
ATOM	613	CD	PRO	A	293	-2.802	74.096	43.247	1.00	42.59
ATOM	614	CA	PRO	A	293	-4.279	72.420	44.237	1.00	41.91
ATOM	615	CB	PRO	A	293	-4.605	73.784	44.806	1.00	41.79
ATOM	616	CG	PRO	A	293	-3.481	74.676	44.450	1.00	41.90
ATOM	617	C	PRO	A	293	-5.441	71.807	43.474	1.00	41.40
ATOM	618	O	PRO	A	293	-5.696	72.212	42.339	1.00	41.02
ATOM	619	N	GLY	A	294	-6.059	70.755	44.003	1.00	40.85
ATOM	620	CA	GLY	A	294	-7.176	70.123	43.332	1.00	41.30
ATOM	621	C	GLY	A	294	-6.832	69.033	42.332	1.00	40.98
ATOM	622	O	GLY	A	294	-7.688	68.185	42.061	1.00	41.17
ATOM	623	N	GLU	A	295	-5.636	69.051	41.753	1.00	39.55
ATOM	624	OE2	GLU	A	295	-2.049	69.989	38.852	1.00	44.47
ATOM	625	OE1	GLU	A	295	-3.356	71.223	37.568	1.00	44.87
ATOM	626	CD	GLU	A	295	-3.176	70.330	38.422	1.00	44.01
ATOM	627	CG	GLU	A	295	-4.422	69.647	38.946	1.00	42.26
ATOM	628	CB	GLU	A	295	-4.099	68.521	39.886	1.00	39.91
ATOM	629	CA	GLU	A	295	-5.214	68.044	40.813	1.00	38.60
ATOM	630	C	GLU	A	295	-4.641	66.825	41.552	1.00	36.59
ATOM	631	O	GLU	A	295	-4.281	66.871	42.720	1.00	36.85
ATOM	632	N	LYS	A	296	-4.418	65.777	40.773	1.00	33.95
ATOM	633	CA	LYS	A	296	-3.782	64.575	41.294	1.00	30.68
ATOM	634	CB	LYS	A	296	-4.755	63.656	41.996	1.00	31.56
ATOM	635	CG	LYS	A	296	-5.992	63.312	41.185	1.00	32.22

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	636	CD	LYS	A	296	-7.149	62.924	42.075	1.00	32.13
ATOM	637	CE	LYS	A	296	-8.161	62.034	41.381	1.00	33.43
ATOM	638	NZ	LYS	A	296	-8.106	62.091	39.904	1.00	34.90
ATOM	639	C	LYS	A	296	-3.028	63.883	40.167	1.00	28.79
ATOM	640	O	LYS	A	296	-3.275	64.112	38.986	1.00	27.50
ATOM	641	N	HIS	A	297	-1.999	63.135	40.580	1.00	25.20
ATOM	642	CA	HIS	A	297	-1.216	62.396	39.584	1.00	20.71
ATOM	643	CB	HIS	A	297	-0.148	63.267	38.981	1.00	20.06
ATOM	644	CG	HIS	A	297	0.824	62.612	38.054	1.00	18.56
ATOM	645	CD2	HIS	A	297	1.808	61.741	38.309	1.00	15.40
ATOM	646	ND1	HIS	A	297	0.863	62.878	36.701	1.00	18.13
ATOM	647	CE1	HIS	A	297	1.844	62.180	36.160	1.00	17.97
ATOM	648	NE2	HIS	A	297	2.416	61.463	37.105	1.00	19.72
ATOM	649	C	HIS	A	297	-0.730	61.151	40.292	1.00	19.15
ATOM	650	O	HIS	A	297	-0.477	61.256	41.493	1.00	18.54
ATOM	651	N	TYR	A	298	-0.557	60.030	39.580	1.00	18.21
ATOM	652	CA	TYR	A	298	-0.155	58.824	40.330	1.00	16.80
ATOM	653	CB	TYR	A	298	-0.193	57.594	39.437	1.00	16.24
ATOM	654	CG	TYR	A	298	0.940	57.509	38.444	1.00	17.23
ATOM	655	CD1	TYR	A	298	2.077	56.755	38.742	1.00	15.56
ATOM	656	CE1	TYR	A	298	3.094	56.667	37.821	1.00	15.21
ATOM	657	CD2	TYR	A	298	0.881	58.184	37.236	1.00	16.74
ATOM	658	CE2	TYR	A	298	1.913	58.098	36.337	1.00	16.91
ATOM	659	CZ	TYR	A	298	3.022	57.325	36.636	1.00	16.49
ATOM	660	OH	TYR	A	298	4.046	57.260	35.719	1.00	18.10
ATOM	661	C	TYR	A	298	1.185	58.981	41.029	1.00	16.63
ATOM	662	O	TYR	A	298	1.351	58.330	42.073	1.00	16.70
ATOM	663	N	ASN	A	299	2.112	59.766	40.523	1.00	16.99
ATOM	664	CA	ASN	A	299	3.423	60.011	41.085	1.00	18.59
ATOM	665	CB	ASN	A	299	4.463	60.166	39.965	1.00	18.92
ATOM	666	CG	ASN	A	299	5.890	60.214	40.494	1.00	18.76
ATOM	667	OD1	ASN	A	299	6.205	59.456	41.412	1.00	18.23
ATOM	668	ND2	ASN	A	299	6.748	61.070	39.950	1.00	19.19
ATOM	669	C	ASN	A	299	3.513	61.224	42.009	1.00	20.06
ATOM	670	O	ASN	A	299	4.606	61.723	42.362	1.00	18.80
ATOM	671	N	MET	A	300	2.395	61.732	42.509	1.00	20.80
ATOM	672	CA	MET	A	300	2.449	62.886	43.417	1.00	22.77
ATOM	673	CB	MET	A	300	1.115	63.568	43.608	1.00	23.16
ATOM	674	CG	MET	A	300	0.029	62.931	44.436	1.00	25.10
ATOM	675	SD	MET	A	300	-1.590	63.723	44.020	1.00	28.00
ATOM	676	CE	MET	A	300	-2.640	62.839	45.144	1.00	24.04
ATOM	677	C	MET	A	300	3.012	62.458	44.767	1.00	21.89
ATOM	678	O	MET	A	300	2.833	61.314	45.160	1.00	18.53
ATOM	679	N	ALA	A	301	3.369	63.413	45.606	1.00	22.83
ATOM	680	CA	ALA	A	301	3.872	63.134	46.926	1.00	23.87
ATOM	681	CB	ALA	A	301	4.450	64.429	47.484	1.00	23.72
ATOM	682	C	ALA	A	301	2.841	62.580	47.893	1.00	24.63
ATOM	683	O	ALA	A	301	3.085	61.615	48.637	1.00	23.46
ATOM	684	N	LYS	A	302	1.652	63.178	47.913	1.00	26.09
ATOM	685	CA	LYS	A	302	0.645	62.719	48.859	1.00	26.00
ATOM	686	CB	LYS	A	302	-0.215	63.890	49.329	1.00	28.38
ATOM	687	CG	LYS	A	302	0.554	65.188	49.528	1.00	29.29
ATOM	688	CD	LYS	A	302	1.697	65.125	50.505	1.00	30.98
ATOM	689	CE	LYS	A	302	2.522	66.407	50.512	1.00	32.65

	Atom Type		Residue	?	#	X	Y	Z	OCC	B
ATOM	690	NZ	LYS	A	302	2.617	67.085	49.191	1.00	33.62
ATOM	691	C	LYS	A	302	-0.198	61.580	48.291	1.00	25.55
ATOM	692	O	LYS	A	302	-0.295	61.399	47.087	1.00	24.72
ATOM	693	N	SER	A	303	-0.793	60.835	49.202	1.00	24.45
ATOM	694	CA	SER	A	303	-1.621	59.696	48.836	1.00	25.50
ATOM	695	CB	SER	A	303	-1.434	58.619	49.878	1.00	26.64
ATOM	696	OG	SER	A	303	-1.869	59.030	51.149	1.00	31.03
ATOM	697	C	SER	A	303	-3.052	60.182	48.666	1.00	25.87
ATOM	698	O	SER	A	303	-3.396	61.256	49.185	1.00	22.73
ATOM	699	N	TYR	A	304	-3.814	59.454	47.855	1.00	24.98
ATOM	700	CA	TYR	A	304	-5.181	59.862	47.550	1.00	24.27
ATOM	701	CB	TYR	A	304	-5.140	60.449	46.132	1.00	25.45
ATOM	702	CG	TYR	A	304	-6.466	61.015	45.686	1.00	28.35
ATOM	703	CD1	TYR	A	304	-6.762	62.357	45.929	1.00	29.08
ATOM	704	CE1	TYR	A	304	-7.978	62.891	45.552	1.00	29.59
ATOM	705	CD2	TYR	A	304	-7.426	60.214	45.085	1.00	27.54
ATOM	706	CE2	TYR	A	304	-8.630	60.754	44.702	1.00	29.33
ATOM	707	CZ	TYR	A	304	-8.893	62.094	44.944	1.00	29.27
ATOM	708	OH	TYR	A	304	-10.103	62.610	44.578	1.00	32.08
ATOM	709	C	TYR	A	304	-6.192	58.769	47.721	1.00	25.14
ATOM	710	O	TYR	A	304	-5.707	57.735	47.336	1.α00	20.08
ATOM	711	N	PRO	A	305	-7.356	59.000	48.279	1.00	26.60
ATOM	712	CD	PRO	A	305	-8.386	58.001	48.459	1.00	25.22
ATOM	713	CA	PRO	A	305	-7.989	60.240	48.637	1.00	27.02
ATOM	714	CB	PRO	A	305	-9.492	60.083	48.491	1.00	25.75
ATOM	715	CG	PRO	A	305	-9.707	58.646	48.789	1.00	25.74
ATOM	716	C	PRO	A	305	-7.625	60.782	50.007	1.00	28.63
ATOM	717	O	PRO	A	305	-7.922	61.915	50.430	1.00	28.68
ATOM	718	N	ASN	A	306	-6.988	59.904	50.783	1.00	29.14
ATOM	719	CA	ASN	A	306	-6.713	60.273	52.173	1.00	30.26
ATOM	720	CB	ASN	A	306	-7.350	59.232	53.075	1.00	32.58
ATOM	721	CG	ASN	A	306	-8.766	58.861	52.676	1.00	35.48
ATOM	722	OD1	ASN	A	306	-9.661	59.712	52.612	1.00	36.24
ATOM	723	ND2	ASN	A	306	-8.992	57.588	52.368	1.00	36.01
ATOM	724	C	ASN	A	306	-5.229	60.477	52.375	1.00	29.94
ATOM	725	O	ASN	A	306	-4.444	59.536	52.439	1.00	28.29
ATOM	726	N	GLU	A	307	-4.819	61.724	52.507	1.00	29.94
ATOM	727	OE2	GLU	A	307	-2.295	66.669	51.130	1.00	41.44
ATOM	728	OE1	GLU	A	307	-2.711	66.223	53.238	1.00	41.35
ATOM	729	CD	GLU	A	307	-2.656	65.896	52.037	1.00	40.02
ATOM	730	CG	GLU	A	307	-3.034	64.464	51.678	1.00	38.20
ATOM	731	CB	GLU	A	307	-3.401	63.683	52.914	1.00	33.77
ATOM	732	CA	GLU	A	307	-3.461	62.152	52.717	1.00	32.32
ATOM	733	C	GLU	A	307	-2.770	61.594	53.949	1.00	30.24
ATOM	734	O	GLU	A	307	-1.542	61.522	53.970	1.00	30.44
ATOM	735	N	GLU	A	308	-3.513	61.273	54.984	1.00	29.39
ATOM	736	OE2	GLU	A	308	-6.099	61.320	55.501	1.00	38.47
ATOM	737	OE1	GLU	A	308	-7.129	59.531	56.089	1.00	37.95
ATOM	738	CD	GLU	A	308	-6.176	60.330	56.250	1.00	36.70
ATOM	739	CG	GLU	A	308	-5.168	60.057	57.322	1.00	35.39
ATOM	740	CB	GLU	A	308	-3.931	60.913	57.384	1.00	33.10
ATOM	741	CA	GLU	A	308	-2.950	60.795	56.224	1.00	29.98
ATOM	742	C	GLU	A	308	-2.487	59.353	56.093	1.00	28.21
ATOM	743	O	GLU	A	308	-1.607	58.963	56.857	1.00	26.31

	Atom Type	Residue	C	#	X	Y	Z	OCC	B
ATOM 744	N	LYS	A	309	-3.004	58.626	55.094	1.00	24.19
ATOM 745	CA	LYS	A	309	-2.648	57.216	55.015	1.00	24.20
ATOM 746	CB	LYS	A	309	-3.711	56.413	54.263	1.00	24.89
ATOM 747	CG	LYS	A	309	-5.098	56.344	54.884	1.00	27.73
ATOM 748	CD	LYS	A	309	-5.089	56.571	56.361	1.00	31.22
ATOM 749	CE	LYS	A	309	-6.317	56.792	57.162	1.00	32.52
ATOM 750	NZ	LYS	A	309	-6.638	55.694	58.107	1.00	34.53
ATOM 751	C	LYS	A	309	-1.285	57.012	54.387	1.00	21.98
ATOM 752	O	LYS	A	309	-0.832	57.851	53.636	1.00	22.27
ATOM 753	N	ASP	A	310	-0.675	55.855	54.593	1.00	20.75
ATOM 754	CA	ASP	A	310	0.605	55.530	53.953	1.00	20.70
ATOM 755	CB	ASP	A	310	1.130	54.173	54.501	1.00	20.19
ATOM 756	CG	ASP	A	310	2.615	54.085	54.167	1.00	22.21
ATOM 757	OD1	ASP	A	310	3.335	54.893	54.831	1.00	24.55
ATOM 758	OD2	ASP	A	310	3.040	53.306	53.292	1.00	18.20
ATOM 759	C	ASP	A	310	0.474	55.419	52.450	1.00	19.43
ATOM 760	O	ASP	A	310	1.385	55.706	51.651	1.00	20.19
ATOM 761	N	ALA	A	311	-0.727	55.044	51.990	1.00	18.69
ATOM 762	CA	ALA	A	311	-0.947	54.834	50.572	1.00	17.44
ATOM 763	CB	ALA	A	311	-0.991	53.296	50.429	1.00	16.55
ATOM 764	C	ALA	A	311	-2.302	55.316	50.028	1.00	16.60
ATOM 765	O	ALA	A	311	-3.221	55.655	50.751	1.00	12.08
ATOM 766	N	TRP	A	312	-2.339	55.302	48.711	1.00	17.19
ATOM 767	CA	TRP	A	312	-3.555	55.615	47.963	1.00	15.85
ATOM 768	CB	TRP	A	312	-3.236	55.569	46.483	1.00	14.37
ATOM 769	CG	TRP	A	312	-2.713	56.757	45.760	1.00	16.10
ATOM 770	CD2	TRP	A	312	-3.413	57.526	44.772	1.00	16.24
ATOM 771	CE2	TRP	A	312	-2.554	58.554	44.342	1.00	17.46
ATOM 772	CE3	TRP	A	312	-4.685	57.427	44.204	1.00	17.59
ATOM 773	CD1	TRP	A	312	-1.492	57.360	45.884	1.00	15.52
ATOM 774	NE1	TRP	A	312	-1.381	58.440	45.050	1.00	16.75
ATOM 775	CZ2	TRP	A	312	-2.900	59.475	43.357	1.00	17.80
ATOM 776	CZ3	TRP	A	312	-5.022	58.348	43.228	1.00	15.80
ATOM 777	CH2	TRP	A	312	-4.154	59.345	42.828	1.00	17.23
ATOM 778	C	TRP	A	312	-4.562	54.502	48.204	1.00	16.18
ATOM 779	O	TRP	A	312	-4.185	53.393	48.559	1.00	14.62
ATOM 780	N	ASP	A	313	-5.841	54.750	47.906	1.00	17.14
ATOM 781	CA	ASP	A	313	-6.817	53.682	47.741	1.00	17.42
ATOM 782	CB	ASP	A	313	-8.170	54.298	47.343	1.00	19.70
ATOM 783	CG	ASP	A	313	-9.106	53.244	46.797	1.00	22.89
ATOM 784	OD1	ASP	A	313	-9.073	52.935	45.598	1.00	24.60
ATOM 785	OD2	ASP	A	313	-9.841	52.697	47.623	1.00	26.78
ATOM 786	C	ASP	A	313	-6.273	52.903	46.539	1.00	14.58
ATOM 787	O	ASP	A	313	-6.033	53.570	45.533	1.00	14.85
ATOM 788	N	VAL	A	314	-6.101	51.596	46.588	1.00	15.33
ATOM 789	CA	VAL	A	314	-5.434	50.915	45.475	1.00	14.25
ATOM 790	CB	VAL	A	314	-5.067	49.478	45.891	1.00	13.94
ATOM 791	CG1	VAL	A	314	-6.266	48.578	46.107	1.00	12.58
ATOM 792	CG2	VAL	A	314	-4.090	48.891	44.864	1.00	12.94
ATOM 793	C	VAL	A	314	-6.110	50.966	44.129	1.00	14.22
ATOM 794	O	VAL	A	314	-5.480	51.152	43.099	1.00	13.01
ATOM 795	N	LYS	A	315	-7.435	50.819	44.092	1.00	16.35
ATOM 796	NZ	LYS	A	315	-12.342	48.884	46.668	1.00	27.78
ATOM 797	CE	LYS	A	315	-11.908	48.279	45.365	1.00	26.99

	Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	798	CD	LYS	A	315	-11.499	49.287	44.334	1.00	24.72
ATOM	799	CG	LYS	A	315	-10.084	49.278	43.775	1.00	21.52
ATOM	800	CB	LYS	A	315	-9.700	50.621	43.204	1.00	18.30
ATOM	801	CA	LYS	A	315	-8.223	50.882	42.870	1.00	17.01
ATOM	802	C	LYS	A	315	-8.111	52.273	42.255	1.00	15.42
ATOM	803	O	LYS	A	315	-7.967	52.432	41.065	1.00	14.82
ATOM	804	N	MET	A	316	-8.189	53.317	43.095	1.00	16.67
ATOM	805	CA	MET	A	316	-8.023	54.673	42.531	1.00	16.96
ATOM	806	CB	MET	A	316	-8.396	55.717	43.579	1.00	19.66
ATOM	807	CG	MET	A	316	-9.874	55.616	43.966	1.00	21.49
ATOM	808	SD	MET	A	316	-10.303	56.858	45.216	1.00	25.95
ATOM	809	CE	MET	A	316	-11.921	56.212	45.655	1.00	23.70
ATOM	810	C	MET	A	316	-6.624	54.927	41.996	1.00	16.13
ATOM	811	O	MET	A	316	-6.463	55.672	41.038	1.00	16.38
ATOM	812	N	LEU	A	317	-5.583	54.315	42.552	1.00	15.29
ATOM	813	CA	LEU	A	317	-4.218	54.490	42.078	1.00	13.26
ATOM	814	CB	LEU	A	317	-3.200	53.915	43.097	1.00	11.74
ATOM	815	CG	LEU	A	317	-1.733	54.036	42.672	1.00	12.04
ATOM	816	CD1	LEU	A	317	-1.323	55.505	42.512	1.00	10.99
ATOM	817	CD2	LEU	A	317	-0.861	53.326	43.698	1.00	11.54
ATOM	818	C	LEU	A	317	-4.079	53.785	40.755	1.00	12.38
ATOM	819	O	LEU	A	317	-3.526	54.334	39.819	1.00	14.48
ATOM	820	N	LEU	A	318	-4.637	52.580	40.616	1.00	12.87
ATOM	821	CA	LEU	A	318	-4.561	51.890	39.326	1.00	12.84
ATOM	822	CB	LEU	A	318	-5.112	50.457	39.453	1.00	12.79
ATOM	823	CG	LEU	A	318	-4.966	49.629	38.170	1.00	14.82
ATOM	824	CD1	LEU	A	318	-3.531	49.542	37.700	1.00	15.86
ATOM	825	CD2	LEU	A	318	-5.558	48.241	38.355	1.00	14.73
ATOM	826	C	LEU	A	318	-5.230	52.673	38.218	1.00	12.07
ATOM	827	O	LEU	A	318	-4.780	52.829	37.099	1.00	12.74
ATOM	828	N	GLU	A	319	-6.420	53.193	38.511	1.00	15.24
ATOM	829	OE2	GLU	A	319	-11.483	52.210	39.220	1.00	28.26
ATOM	830	OE1	GLU	A	319	-10.797	54.093	40.042	1.00	29.42
ATOM	831	CD	GLU	A	319	-10.674	53.181	39.193	1.00	27.45
ATOM	832	CG	GLU	A	319	-9.561	53.233	38.177	1.00	24.55
ATOM	833	CB	GLU	A	319	-8.553	54.375	38.270	1.00	18.18
ATOM	834	CA	GLU	A	319	-7.199	54.025	37.614	1.00	15.25
ATOM	835	C	GLU	A	319	-6.421	55.288	37.289	1.00	14.06
ATOM	836	O	GLU	A	319	-6.317	55.697	36.141	1.00	13.57
ATOM	837	N	GLN	A	320	-5.879	55.947	38.303	1.00	14.48
ATOM	838	CA	GLN	A	320	-5.086	57.164	38.073	1.00	15.95
ATOM	839	CB	GLN	A	320	-4.631	57.772	39.413	1.00	17.37
ATOM	840	CG	GLN	A	320	-3.969	59.147	39.262	1.00	20.30
ATOM	841	CD	GLN	A	320	-4.917	60.189	38.681	1.00	20.82
ATOM	842	OE1	GLN	A	320	-6.069	60.198	39.101	1.00	22.55
ATOM	843	NE2	GLN	A	320	-4.480	61.016	37.768	1.00	20.50
ATOM	844	C	GLN	A	320	-3.896	56.849	37.206	1.00	15.14
ATOM	845	O	GLN	A	320	-3.545	57.572	36.274	1.00	16.35
ATOM	846	N	PHE	A	321	-3.178	55.751	37.535	1.00	14.19
ATOM	847	CA	PHE	A	321	-1.997	55.416	36.728	1.00	13.62
ATOM	848	CB	PHE	A	321	-1.389	54.100	37.277	1.00	14.84
ATOM	849	CG	PHE	A	321	-0.286	53.531	36.462	1.00	14.25
ATOM	850	CD1	PHE	A	321	0.874	54.232	36.256	1.00	16.53
ATOM	851	CD2	PHE	A	321	-0.407	52.275	35.889	1.00	15.71

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	852	CE1	PHE	A	321	1.915	53.714	35.499	1.00	16.96
ATOM	853	CE2	PHE	A	321	0.594	51.737	35.109	1.00	16.98
ATOM	854	CZ	PHE	A	321	1.760	52.464	34.920	1.00	19.64
ATOM	855	C	PHE	A	321	-2.367	55.265	35.284	1.00	15.37
ATOM	856	O	PHE	A	321	-1.743	55.838	34.391	1.00	17.95
ATOM	857	N	SER	A	322	-3.440	54.502	35.011	1.00	15.65
ATOM	858	CA	SER	A	322	-3.862	54.261	33.650	1.00	16.47
ATOM	859	CB	SER	A	322	-5.052	53.312	33.545	1.00	17.62
ATOM	860	OG	SER	A	322	-4.956	52.111	34.281	1.00	21.90
ATOM	861	C	SER	A	322	-4.219	55.608	32.980	1.00	15.02
ATOM	862	O	SER	A	322	-3.836	55.773	31.839	1.00	15.73
ATOM	863	N	PHE	A	323	-4.855	56.499	33.694	1.00	15.76
ATOM	864	CA	PHE	A	323	-5.163	57.831	33.153	1.00	17.15
ATOM	865	CB	PHE	A	323	-5.953	58.697	34.136	1.00	18.22
ATOM	866	CG	PHE	A	323	-6.374	60.050	33.604	1.00	20.68
ATOM	867	CD1	PHE	A	323	-5.660	61.195	33.861	1.00	21.45
ATOM	868	CD2	PHE	A	323	-7.524	60.161	32.852	1.00	22.31
ATOM	869	CE1	PHE	A	323	-6.032	62.425	33.329	1.00	22.60
ATOM	870	CE2	PHE	A	323	-7.945	61.384	32.325	1.00	24.15
ATOM	871	CZ	PHE	A	323	-7.175	62.502	32.558	1.00	23.26
ATOM	872	C	PHE	A	323	-3.897	58.570	32.756	1.00	18.08
ATOM	873	O	PHE	A	323	-3.807	59.053	31.648	1.00	15.95
ATOM	874	N	ASP	A	324	-2.913	58.698	33.662	1.00	19.20
ATOM	875	CA	ASP	A	324	-1.748	59.521	33.405	1.00	20.57
ATOM	876	CB	ASP	A	324	-0.994	59.740	34.742	1.00	23.05
ATOM	877	CG	ASP	A	324	-1.773	60.624	35.687	1.00	23.08
ATOM	878	OD1	ASP	A	324	-1.894	60.419	36.896	1.00	22.69
ATOM	879	OD2	ASP	A	324	-2.335	61.620	35.188	1.00	26.34
ATOM	880	C	ASP	A	324	-0.746	58.999	32.402	1.00	21.82
ATOM	881	O	ASP	A	324	-0.058	59.793	31.764	1.00	21.73
ATOM	882	N	ILE	A	325	-0.672	57.679	32.240	1.00	21.33
ATOM	883	CA	ILE	A	325	0.264	57.038	31.339	1.00	22.61
ATOM	884	CB	ILE	A	325	0.922	55.889	32.161	1.00	25.69
ATOM	885	CG2	ILE	A	325	0.154	54.579	32.043	1.00	24.65
ATOM	886	CG1	ILE	A	325	2.370	55.730	31.765	1.00	26.90
ATOM	887	CD1	ILE	A	325	3.369	56.465	32.631	1.00	27.55
ATOM	888	C	ILE	A	325	-0.394	56.551	30.073	1.00	22.34
ATOM	889	O	ILE	A	325	0.238	55.950	29.209	1.00	19.22
ATOM	890	N	ALA	A	326	-1.663	56.970	29.849	1.00	21.30
ATOM	891	CA	ALA	A	326	-2.412	56.538	28.677	1.00	21.14
ATOM	892	CB	ALA	A	326	-3.743	57.301	28.568	1.00	20.96
ATOM	893	C	ALA	A	326	-1.701	56.616	27.350	1.00	20.02
ATOM	894	O	ALA	A	326	-1.716	55.660	26.557	1.00	18.13
ATOM	895	N	GLU	A	327	-1.087	57.750	27.055	1.00	21.17
ATOM	896	OE2	GLU	A	327	1.606	59.498	22.827	1.00	38.00
ATOM	897	OE1	GLU	A	327	-0.468	59.073	22.310	1.00	37.16
ATOM	898	CD	GLU	A	327	0.389	59.482	23.114	1.00	35.40
ATOM	899	CG	GLU	A	327	-0.062	59.993	24.456	1.00	33.57
ATOM	900	CB	GLU	A	327	0.333	59.223	25.685	1.00	26.72
ATOM	901	CA	GLU	A	327	-0.310	57.845	25.805	1.00	23.82
ATOM	902	C	GLU	A	327	0.748	56.760	25.705	1.00	20.97
ATOM	903	O	GLU	A	327	0.932	56.156	24.626	1.00	20.68
ATOM	904	N	GLU	A	328	1.536	56.501	26.758	1.00	20.00
ATOM	905	OE2	GLU	A	328	6.485	57.857	28.558	1.00	20.00

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	906	OE1	GLU	A	328	5.550	56.151	29.650	1.00	20.00
ATOM	907	CD	GLU	A	328	5.561	56.965	28.651	1.00	20.00
ATOM	908	CG	GLU	A	328	4.474	56.875	27.579	1.00	20.00
ATOM	909	CB	GLU	A	328	3.625	55.608	27.694	1.00	20.00
ATOM	910	CA	GLU	A	328	2.584	55.483	26.582	1.00	20.00
ATOM	911	C	GLU	A	328	1.966	54.088	26.633	1.00	20.00
ATOM	912	O	GLU	A	328	2.420	53.176	25.932	1.00	20.00
ATOM	913	N	ALA	A	329	0.930	53.900	27.438	1.00	19.57
ATOM	914	CA	ALA	A	329	0.280	52.586	27.501	1.00	21.09
ATOM	915	CB	ALA	A	329	-0.828	52.628	28.545	1.00	20.52
ATOM	916	C	ALA	A	329	-0.292	52.148	26.167	1.00	21.74
ATOM	917	O	ALA	A	329	-0.460	50.963	25.860	1.00	22.92
ATOM	918	N	SER	A	330	-0.593	53.077	25.263	1.00	22.47
ATOM	919	CA	SER	A	330	-1.185	52.807	23.972	1.00	23.55
ATOM	920	CB	SER	A	330	-1.669	54.151	23.397	1.00	23.31
ATOM	921	OG	SER	A	330	-0.614	54.856	22.781	1.00	25.74
ATOM	922	C	SER	A	330	-0.209	52.129	23.038	1.00	23.79
ATOM	923	O	SER	A	330	-0.545	51.533	22.032	1.00	23.93
ATOM	924	N	LYS	A	331	1.073	52.141	23.385	1.00	20.00
ATOM	925	NZ	LYS	A	331	4.948	57.241	21.295	1.00	20.00
ATOM	926	CE	LYS	A	331	3.827	56.290	21.276	1.00	20.00
ATOM	927	CD	LYS	A	331	4.162	54.958	21.950	1.00	20.00
ATOM	928	CG	LYS	A	331	2.995	53.972	21.928	1.00	20.00
ATOM	929	CB	LYS	A	331	3.327	52.639	22.588	1.00	20.00
ATOM	930	CA	LYS	A	331	2.147	51.613	22.574	1.00	20.00
ATOM	931	C	LYS	A	331	2.659	50.261	22.982	1.00	20.00
ATOM	932	O	LYS	A	331	3.484	49.683	22.278	1.00	20.00
ATOM	933	N	VAL	A	332	2.207	49.748	24.112	1.00	21.24
ATOM	934	CA	VAL	A	332	2.660	48.458	24.592	1.00	19.62
ATOM	935	CB	VAL	A	332	3.467	48.639	25.896	1.00	20.18
ATOM	936	CG1	VAL	A	332	4.816	49.290	25.660	1.00	19.67
ATOM	937	CG2	VAL	A	332	2.651	49.433	26.897	1.00	18.82
ATOM	938	C	VAL	A	332	1.495	47.533	24.905	1.00	18.19
ATOM	939	O	VAL	A	332	0.344	47.965	24.964	1.00	18.61
ATOM	940	N	CYS	A	333	1.816	46.274	25.098	1.00	16.72
ATOM	941	CA	CYS	A	333	0.869	45.245	25.475	1.00	18.08
ATOM	942	CB	CYS	A	333	1.522	43.872	25.365	1.00	20.13
ATOM	943	SG	CYS	A	333	0.694	42.448	26.048	1.00	23.29
ATOM	944	C	CYS	A	333	0.346	45.494	26.878	1.00	16.83
ATOM	945	O	CYS	A	333	-0.855	45.347	27.075	1.00	15.63
ATOM	946	N	LEU	A	334	1.226	45.820	27.841	1.00	12.87
ATOM	947	CA	LEU	A	334	0.838	46.094	29.187	1.00	12.88
ATOM	948	CB	LEU	A	334	0.857	44.925	30.157	1.00	13.67
ATOM	949	CG	LEU	A	334	0.004	43.686	29.867	1.00	12.92
ATOM	950	CD1	LEU	A	334	0.432	42.513	30.699	1.00	9.29
ATOM	951	CD2	LEU	A	334	-1.465	44.030	30.158	1.00	10.80
ATOM	952	C	LEU	A	334	1.788	47.151	29.816	1.00	14.90
ATOM	953	O	LEU	A	334	2.929	47.313	29.428	1.00	13.88
ATOM	954	N	ALA	A	335	1.203	47.856	30.778	1.00	14.03
ATOM	955	CA	ALA	A	335	1.920	48.854	31.544	1.00	14.38
ATOM	956	CB	ALA	A	335	1.292	50.235	31.381	1.00	15.95
ATOM	957	C	ALA	A	335	1.859	48.404	32.991	1.00	13.27
ATOM	958	O	ALA	A	335	0.794	48.020	33.435	1.00	14.32
ATOM	959	N	HIS	A	336	2.936	48.458	33.750	1.00	12.02

	Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	960	CA	HIS	A	336	2.886	48.039	35.141	1.00	10.67
ATOM	961	CB	HIS	A	336	3.543	46.655	35.252	1.00	9.55
ATOM	962	CG	HIS	A	336	3.104	45.903	36.449	1.00	12.03
ATOM	963	CD2	HIS	A	336	2.026	45.099	36.601	1.00	9.22
ATOM	964	ND1	HIS	A	336	3.730	45.915	37.684	1.00	11.53
ATOM	965	CE1	HIS	A	336	3.048	45.186	38.533	1.00	8.45
ATOM	966	NE2	HIS	A	336	1.995	44.711	37.891	1.00	12.17
ATOM	967	C	HIS	A	336	3.596	49.089	36.001	1.00	13.40
ATOM	968	O	HIS	A	336	4.669	49.576	35.641	1.00	13.52
ATOM	969	N	LEU	A	337	2.987	49.473	37.104	1.00	12.61
ATOM	970	CA	LEU	A	337	3.514	50.440	38.026	1.00	12.83
ATOM	971	CB	LEU	A	337	2.357	51.336	38.563	1.00	13.25
ATOM	972	CG	LEU	A	337	2.688	52.163	39.816	1.00	14.22
ATOM	973	CD1	LEU	A	337	3.886	53.054	39.540	1.00	14.34
ATOM	974	CD2	LEU	A	337	1.489	53.027	40.232	1.00	12.48
ATOM	975	C	LEU	A	337	4.137	49.730	39.243	1.00	11.76
ATOM	976	O	LEU	A	337	3.486	48.887	39.833	1.00	10.29
ATOM	977	N	PHE	A	338	5.396	50.012	39.548	1.00	11.12
ATOM	978	CA	PHE	A	338	6.001	49.502	40.775	1.00	9.77
ATOM	979	CB	PHE	A	338	7.378	48.877	40.584	1.00	10.95
ATOM	980	CG	PHE	A	338	7.336	47.661	39.688	1.00	10.01
ATOM	981	CD1	PHE	A	338	7.341	47.745	38.336	1.00	6.77
ATOM	982	CD2	PHE	A	338	7.347	46.392	40.263	1.00	10.50
ATOM	983	CE1	PHE	A	338	7.261	46.629	37.530	1.00	8.39
ATOM	984	CE2	PHE	A	338	7.260	45.254	39.504	1.00	7.33
ATOM	985	CZ	PHE	A	338	7.257	45.387	38.135	1.00	9.45
ATOM	986	C	PHE	A	338	6.093	50.673	41.742	1.00	10.02
ATOM	987	O	PHE	A	338	6.621	51.737	41.430	1.00	11.99
ATOM	988	N	THR	A	339	5.501	50.493	42.897	1.00	9.73
ATOM	989	CA	THR	A	339	5.455	51.468	43.940	1.00	12.72
ATOM	990	CB	THR	A	339	4.053	52.092	44.003	1.00	15.30
ATOM	991	OG1	THR	A	339	4.060	53.246	44.828	1.00	16.97
ATOM	992	CG2	THR	A	339	3.048	51.044	44.495	1.00	15.12
ATOM	993	C	THR	A	339	5.886	50.830	45.261	1.00	12.86
ATOM	994	O	THR	A	339	6.169	49.638	45.386	1.00	12.05
ATOM	995	N	TYR	A	340	5.954	51.663	46.268	1.00	11.17
ATOM	996	CA	TYR	A	340	6.323	51.315	47.616	1.00	11.82
ATOM	997	CB	TYR	A	340	7.823	51.632	47.844	1.00	10.81
ATOM	998	CG	TYR	A	340	8.342	51.050	49.121	1.00	11.94
ATOM	999	CD1	TYR	A	340	8.766	49.717	49.157	1.00	13.34
ATOM	1000	CE1	TYR	A	340	9.228	49.144	50.342	1.00	13.22
ATOM	1001	CD2	TYR	A	340	8.375	51.795	50.286	1.00	11.57
ATOM	1002	CE2	TYR	A	340	8.862	51.239	51.481	1.00	13.34
ATOM	1003	CZ	TYR	A	340	9.294	49.929	51.474	1.00	12.53
ATOM	1004	OH	TYR	A	340	9.708	49.349	52.630	1.00	13.01
ATOM	1005	C	TYR	A	340	5.422	52.066	48.560	1.00	12.56
ATOM	1006	O	TYR	A	340	5.784	53.138	49.086	1.00	13.24
ATOM	1007	N	GLN	A	341	4.248	51.479	48.801	1.00	12.63
ATOM	1008	CA	GLN	A	341	3.279	52.124	49.697	1.00	12.73
ATOM	1009	CB	GLN	A	341	2.457	53.199	48.996	1.00	15.96
ATOM	1010	CG	GLN	A	341	1.630	52.745	47.790	1.00	12.86
ATOM	1011	CD	GLN	A	341	1.063	53.915	47.015	1.00	14.37
ATOM	1012	OE1	GLN	A	341	0.019	54.455	47.412	1.00	14.26
ATOM	1013	NE2	GLN	A	341	1.690	54.336	45.913	1.00	12.87

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1014	C	GLN	A	341	2.409	51.026	50.281	1.00	13.05
ATOM	1015	O	GLN	A	341	2.135	50.001	49.651	1.00	12.36
ATOM	1016	N	ASP	A	342	2.036	51.214	51.518	1.00	11.62
ATOM	1017	CA	ASP	A	342	1.313	50.221	52.293	1.00	12.36
ATOM	1018	CB	ASP	A	342	1.766	50.350	53.748	1.00	11.58
ATOM	1019	CG	ASP	A	342	1.603	49.084	54.533	1.00	14.83
ATOM	1020	OD1	ASP	A	342	1.136	48.053	53.979	1.00	12.25
ATOM	1021	OD2	ASP	A	342	1.976	49.034	55.734	1.00	16.16
ATOM	1022	C	ASP	A	342	-0.202	50.344	52.159	1.00	13.76
ATOM	1023	O	ASP	A	342	-0.850	50.940	53.016	1.00	10.06
ATOM	1024	N	PHE	A	343	-0.705	49.804	51.047	1.00	12.77
ATOM	1025	CA	PHE	A	343	-2.123	49.686	50.828	1.00	13.67
ATOM	1026	CB	PHE	A	343	-2.407	48.846	49.572	1.00	11.23
ATOM	1027	CG	PHE	A	343	-1.813	49.447	48.336	1.00	13.10
ATOM	1028	CD1	PHE	A	343	-2.070	50.761	47.978	1.00	11.42
ATOM	1029	CD2	PHE	A	343	-0.968	48.703	47.519	1.00	11.91
ATOM	1030	CE1	PHE	A	343	-1.494	51.298	46.845	1.00	11.83
ATOM	1031	CE2	PHE	A	343	-0.431	49.235	46.395	1.00	13.17
ATOM	1032	CZ	PHE	A	343	-0.693	50.547	46.011	1.00	11.97
ATOM	1033	C	PHE	A	343	-2.827	49.073	52.018	1.00	13.82
ATOM	1034	O	PHE	A	343	-2.411	48.111	52.663	1.00	11.97
ATOM	1035	N	ASP	A	344	-3.976	49.646	52.364	1.00	14.70
ATOM	1036	CA	ASP	A	344	-4.734	49.159	53.500	1.00	16.30
ATOM	1037	CB	ASP	A	344	-6.066	49.896	53.688	1.00	19.86
ATOM	1038	CG	ASP	A	344	-5.919	51.270	54.287	1.00	24.51
ATOM	1039	OD1	ASP	A	344	-4.851	51.804	54.586	1.00	24.70
ATOM	1040	OD2	ASP	A	344	-6.983	51.916	54.436	1.00	27.18
ATOM	1041	C	ASP	A	344	-5.093	47.675	53.396	1.00	13.85
ATOM	1042	O	ASP	A	344	-5.208	47.157	52.310	1.00	9.77
ATOM	1043	N	MET	A	345	-5.213	47.069	54.564	1.00	13.16
ATOM	1044	CA	MET	A	345	-5.708	45.753	54.800	1.00	17.11
ATOM	1045	CB	MET	A	345	-7.235	45.710	54.450	1.00	23.01
ATOM	1046	CG	MET	A	345	-7.944	46.687	55.406	1.00	28.99
ATOM	1047	SD	MET	A	345	-9.349	45.913	56.215	1.00	39.05
ATOM	1048	CE	MET	A	345	-9.993	47.308	57.172	1.00	36.28
ATOM	1049	C	MET	A	345	-4.992	44.658	54.023	1.00	16.11
ATOM	1050	O	MET	A	345	-5.586	43.729	53.496	1.00	11.01
ATOM	1051	N	GLY	A	346	-3.649	44.811	53.976	1.00	13.02
ATOM	1052	CA	GLY	A	346	-2.848	43.775	53.364	1.00	12.48
ATOM	1053	C	GLY	A	346	-2.754	43.637	51.897	1.00	10.57
ATOM	1054	O	GLY	A	346	-2.092	42.654	51.492	1.00	10.20
ATOM	1055	N	THR	A	347	-3.392	44.516	51.092	1.00	10.34
ATOM	1056	CA	THR	A	347	-3.236	44.419	49.645	1.00	10.83
ATOM	1057	CB	THR	A	347	-4.204	45.426	48.958	1.00	11.57
ATOM	1058	OG1	THR	A	347	-5.515	45.104	49.474	1.00	11.02
ATOM	1059	CG2	THR	A	347	-4.265	45.214	47.479	1.00	9.59
ATOM	1060	C	THR	A	347	-1.836	44.663	49.119	1.00	11.95
ATOM	1061	O	THR	A	347	-1.160	45.651	49.506	1.00	10.72
ATOM	1062	N	LEU	A	348	-1.400	43.853	48.171	1.00	9.29
ATOM	1063	CA	LEU	A	348	-0.082	43.950	47.585	1.00	11.62
ATOM	1064	CB	LEU	A	348	0.550	42.518	47.580	1.00	11.68
ATOM	1065	CG	LEU	A	348	0.940	41.992	48.967	1.00	13.21
ATOM	1066	CD1	LEU	A	348	1.053	40.466	48.924	1.00	13.82
ATOM	1067	CD2	LEU	A	348	2.282	42.599	49.398	1.00	13.80

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1068	C	LEU	A	348	-0.066	44.478	46.170	1.00	10.88
ATOM	1069	O	LEU	A	348	0.889	45.107	45.724	1.00	10.81
ATOM	1070	N	GLY	A	349	-1.177	44.229	45.417	1.00	10.78
ATOM	1071	CA	GLY	A	349	-1.154	44.718	44.035	1.00	9.96
ATOM	1072	C	GLY	A	349	-2.577	44.686	43.420	1.00	11.05
ATOM	1073	O	GLY	A	349	-3.461	44.195	44.075	1.00	9.57
ATOM	1074	N	LEU	A	350	-2.667	45.177	42.201	1.00	12.61
ATOM	1075	CA	LEU	A	350	-4.033	45.102	41.592	1.00	12.78
ATOM	1076	CB	LEU	A	350	-4.766	46.348	42.090	1.00	13.89
ATOM	1077	CG	LEU	A	350	-6.279	46.356	41.850	1.00	16.31
ATOM	1078	CD1	LEU	A	350	-6.981	45.416	42.807	1.00	17.00
ATOM	1079	CD2	LEU	A	350	-6.786	47.797	41.945	1.00	15.79
ATOM	1080	C	LEU	A	350	-3.881	45.086	40.119	1.00	10.61
ATOM	1081	O	LEU	A	350	-2.867	45.625	39.674	1.00	9.12
ATOM	1082	N	ALA	A	351	-4.815	44.544	39.319	1.00	8.13
ATOM	1083	CA	ALA	A	351	-4.645	44.560	37.896	1.00	9.68
ATOM	1084	CB	ALA	A	351	-3.807	43.358	37.429	1.00	8.30
ATOM	1085	C	ALA	A	351	-6.006	44.393	37.158	1.00	8.00
ATOM	1086	O	ALA	A	351	-6.781	43.671	37.749	1.00	8.17
ATOM	1087	N	TYR	A	352	-6.102	44.923	35.997	1.00	10.56
ATOM	1088	CA	TYR	A	352	-7.378	44.669	35.243	1.00	11.99
ATOM	1089	CB	TYR	A	352	-7.517	45.727	34.152	1.00	13.49
ATOM	1090	CG	TYR	A	352	-7.816	47.102	34.704	1.00	16.49
ATOM	1091	CD1	TYR	A	352	-9.085	47.388	35.198	1.00	18.25
ATOM	1092	CE1	TYR	A	352	-9.369	48.643	35.704	1.00	18.58
ATOM	1093	CD2	TYR	A	352	-6.835	48.096	34.726	1.00	15.80
ATOM	1094	CE2	TYR	A	352	-7.121	49.344	35.231	1.00	17.33
ATOM	1095	CZ	TYR	A	352	-8.385	49.612	35.726	1.00	19.62
ATOM	1096	OH	TYR	A	352	-8.671	50.865	36.229	1.00	20.81
ATOM	1097	C	TYR	A	352	-7.306	43.297	34.623	1.00	11.61
ATOM	1098	O	TYR	A	352	-6.226	42.856	34.133	1.00	9.99
ATOM	1099	N	VAL	A	353	-8.414	42.569	34.618	1.00	9.19
ATOM	1100	CA	VAL	A	353	-8.433	41.240	34.027	1.00	9.63
ATOM	1101	CB	VAL	A	353	-9.532	40.388	34.675	1.00	12.16
ATOM	1102	CG1	VAL	A	353	-9.580	38.963	34.168	1.00	11.71
ATOM	1103	CG2	VAL	A	353	-9.337	40.459	36.180	1.00	11.77
ATOM	1104	C	VAL	A	353	-8.597	41.233	32.532	1.00	12.50
ATOM	1105	O	VAL	A	353	-9.522	41.869	32.012	1.00	12.29
ATOM	1106	N	GLY	A	354	-7.759	40.476	31.830	1.00	10.94
ATOM	1107	CA	GLY	A	354	-7.781	40.328	30.400	1.00	14.31
ATOM	1108	C	GLY	A	354	-8.927	39.377	29.976	1.00	14.67
ATOM	1109	O	GLY	A	354	-9.497	38.711	30.814	1.00	13.50
ATOM	1110	N	SER	A	355	-9.183	39.300	28.685	1.00	15.31
ATOM	1111	CA	SER	A	355	-10.226	38.340	28.254	1.00	18.47
ATOM	1112	CB	SER	A	355	-11.596	39.039	28.449	1.00	19.00
ATOM	1113	OG	SER	A	355	-12.631	38.360	27.760	1.00	21.32
ATOM	1114	C	SER	A	355	-9.959	38.049	26.808	1.00	17.63
ATOM	1115	O	SER	A	355	-9.378	38.937	26.168	1.00	18.38
ATOM	1116	N	PRO	A	356	-10.461	36.952	26.271	1.00	19.06
ATOM	1117	CD	PRO	A	356	-11.125	35.862	27.017	1.00	18.95
ATOM	1118	CA	PRO	A	356	-10.370	36.661	24.859	1.00	21.26
ATOM	1119	CB	PRO	A	356	-10.771	35.200	24.707	1.00	20.19
ATOM	1120	CG	PRO	A	356	-11.451	34.834	25.974	1.00	20.51
ATOM	1121	C	PRO	A	356	-11.357	37.502	24.051	1.00	24.27

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1122	O	PRO	A	356	-11.249	37.622	22.833	1.00	25.16
ATOM	1123	N	ARG	A	357	-12.369	38.028	24.714	1.00	27.47
ATOM	1124	NH2	ARG	A	357	-14.829	39.823	29.846	1.00	45.75
ATOM	1125	NH1	ARG	A	357	-15.278	41.187	28.059	1.00	45.46
ATOM	1126	CZ	ARG	A	357	-15.278	39.980	28.609	1.00	43.96
ATOM	1127	NE	ARG	A	357	-15.708	38.909	27.965	1.00	41.93
ATOM	1128	CD	ARG	A	357	-16.239	38.818	26.627	1.00	38.04
ATOM	1129	CG	ARG	A	357	-15.252	38.219	25.641	1.00	34.46
ATOM	1130	CB	ARG	A	357	-14.476	39.345	24.961	1.00	32.97
ATOM	1131	CA	ARG	A	357	-13.386	38.812	24.032	1.00	31.58
ATOM	1132	C	ARG	A	357	-12.777	39.943	23.231	1.00	33.38
ATOM	1133	O	ARG	A	357	-11.979	40.784	23.635	1.00	32.52
ATOM	1134	CB	ALA	A	358	-13.971	40.872	19.874	1.00	35.32
ATOM	1135	C	ALA	A	358	-12.904	42.350	21.524	1.00	36.30
ATOM	1136	O	ALA	A	358	-11.940	43.090	21.425	1.00	37.79
ATOM	1137	N	ALA	A	358	-13.235	39.948	21.981	1.00	35.10
ATOM	1138	CA	ALA	A	358	-12.901	40.933	20.979	1.00	36.40
ATOM	1139	N	ASN	A	359	-14.027	42.745	22.100	1.00	36.18
ATOM	1140	ND2	ASN	A	359	-17.589	44.247	20.981	1.00	38.54
ATOM	1141	OD1	ASN	A	359	-15.577	44.791	20.178	1.00	40.48
ATOM	1142	CG	ASN	A	359	-16.290	44.493	21.132	1.00	39.04
ATOM	1143	CB	ASN	A	359	-15.760	44.367	22.540	1.00	37.70
ATOM	1144	CA	ASN	A	359	-14.263	44.061	22.641	1.00	36.27
ATOM	1145	C	ASN	A	359	-13.834	44.198	24.094	1.00	35.65
ATOM	1146	O	ASN	A	359	-14.157	45.182	24.751	1.00	35.92
ATOM	1147	N	SER	A	360	-13.119	43.218	24.615	1.00	34.08
ATOM	1148	OG	SER	A	360	-10.429	42.540	26.749	1.00	34.50
ATOM	1149	CB	SER	A	360	-11.683	42.108	26.257	1.00	33.68
ATOM	1150	CA	SER	A	360	-12.647	43.261	25.982	1.00	32.95
ATOM	1151	C	SER	A	360	-11.907	44.577	26.260	1.00	30.62
ATOM	1152	O	SER	A	360	-11.073	45.055	25.505	1.00	29.59
ATOM	1153	N	HIS	A	361	-12.244	45.128	27.405	1.00	28.43
ATOM	1154	CD2	HIS	A	361	-14.316	47.743	26.576	1.00	37.21
ATOM	1155	NE2	HIS	A	361	-14.610	48.664	25.596	1.00	37.98
ATOM	1156	CE1	HIS	A	361	-13.624	49.531	25.503	1.00	37.94
ATOM	1157	ND1	HIS	A	361	-12.729	49.221	26.413	1.00	38.32
ATOM	1158	CG	HIS	A	361	-13.138	48.108	27.110	1.00	36.46
ATOM	1159	CB	HIS	A	361	-12.374	47.488	28.234	1.00	33.76
ATOM	1160	CA	HIS	A	361	-11.550	46.275	27.920	1.00	30.24
ATOM	1161	C	HIS	A	361	-10.928	45.653	29.193	1.00	29.98
ATOM	1162	O	HIS	A	361	-11.660	45.080	30.014	1.00	33.02
ATOM	1163	N	GLY	A	362	-9.625	45.543	29.184	1.00	25.53
ATOM	1164	CA	GLY	A	362	-8.942	45.064	30.371	1.00	20.70
ATOM	1165	C	GLY	A	362	-7.829	44.108	29.983	1.00	16.68
ATOM	1166	O	GLY	A	362	-7.986	43.330	29.056	1.00	12.10
ATOM	1167	N	GLY	A	363	-6.695	44.301	30.672	1.00	13.81
ATOM	1168	CA	GLY	A	363	-5.648	43.339	30.406	1.00	14.18
ATOM	1169	C	GLY	A	363	-4.908	43.513	29.110	1.00	13.66
ATOM	1170	O	GLY	A	363	-4.808	44.608	28.557	1.00	12.16
ATOM	1171	N	VAL	A	364	-4.310	42.413	28.673	1.00	14.17
ATOM	1172	CG2	VAL	A	364	-4.030	40.030	27.062	1.00	15.53
ATOM	1173	CG1	VAL	A	364	-1.902	40.628	28.266	1.00	15.36
ATOM	1174	CB	VAL	A	364	-2.897	41.047	27.174	1.00	18.71
ATOM	1175	CA	VAL	A	364	-3.455	42.442	27.502	1.00	17.47

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1176	C	VAL	A	364	-4.138	43.070	26.294	1.00	22.13
ATOM	1177	O	VAL	A	364	-5.313	42.870	26.039	1.00	18.74
ATOM	1178	N	CYS	A	365	-3.323	43.852	25.611	1.00	26.09
ATOM	1179	SG	CYS	A	365	-3.257	42.201	22.935	1.00	38.70
ATOM	1180	CB	CYS	A	365	-4.184	43.720	23.283	1.00	34.15
ATOM	1181	CA	CYS	A	365	-3.608	44.572	24.400	1.00	32.02
ATOM	1182	C	CYS	A	365	-4.433	45.808	24.719	1.00	32.84
ATOM	1183	O	CYS	A	365	-5.505	45.800	25.307	1.00	33.41
ATOM	1184	N	PRO	A	366	-3.826	46.943	24.391	1.00	34.94
ATOM	1185	CG	PRO	A	366	-2.315	48.596	23.731	1.00	34.57
ATOM	1186	CD	PRO	A	366	-2.542	47.119	23.698	1.00	34.14
ATOM	1187	CB	PRO	A	366	-3.403	49.216	24.501	1.00	35.23
ATOM	1188	CA	PRO	A	366	-4.515	48.220	24.644	1.00	35.75
ATOM	1189	C	PRO	A	366	-5.714	48.244	23.715	1.00	36.16
ATOM	1190	O	PRO	A	366	-5.574	47.917	22.548	1.00	38.73
ATOM	1191	N	LYS	A	367	-6.905	48.420	24.211	1.00	36.55
ATOM	1192	NZ	LYS	A	367	-11.060	46.083	19.713	1.00	39.83
ATOM	1193	CE	LYS	A	367	-10.945	46.830	20.990	1.00	39.58
ATOM	1194	CD	LYS	A	367	-10.461	45.989	22.141	1.00	39.79
ATOM	1195	CG	LYS	A	367	-9.071	46.373	22.617	1.00	39.82
ATOM	1196	CB	LYS	A	367	-9.031	47.227	23.867	1.00	36.78
ATOM	1197	CA	LYS	A	367	-8.228	48.530	23.676	1.00	37.98
ATOM	1198	C	LYS	A	367	-8.995	49.679	24.375	1.00	36.54
ATOM	1199	O	LYS	A	367	-9.725	49.528	25.366	1.00	33.85
ATOM	1200	N	ALA	A	368	-8.855	50.888	23.839	1.00	35.07
ATOM	1201	CA	ALA	A	368	-9.376	52.113	24.400	1.00	32.73
ATOM	1202	CB	ALA	A	368	-9.170	53.209	23.330	1.00	34.00
ATOM	1203	C	ALA	A	368	-10.770	52.317	24.933	1.00	32.95
ATOM	1204	O	ALA	A	368	-11.784	51.928	24.364	1.00	32.14
ATOM	1205	N	TYR	A	369	-10.878	53.117	25.991	1.00	31.03
ATOM	1206	CA	TYR	A	369	-12.087	53.643	26.567	1.00	32.06
ATOM	1207	CB	TYR	A	369	-12.264	53.583	28.057	1.00	34.85
ATOM	1208	CG	TYR	A	369	-13.026	52.465	28.689	1.00	37.47
ATOM	1209	CD1	TYR	A	369	-12.349	51.435	29.321	1.00	38.45
ATOM	1210	CE1	TYR	A	369	-13.025	50.390	29.914	1.00	39.73
ATOM	1211	CD2	TYR	A	369	-14.410	52.415	28.669	1.00	39.08
ATOM	1212	CE2	TYR	A	369	-15.096	51.380	29.271	1.00	40.46
ATOM	1213	CZ	TYR	A	369	-14.397	50.369	29.891	1.00	41.04
ATOM	1214	OH	TYR	A	369	-15.067	49.320	30.483	1.00	42.68
ATOM	1215	C	TYR	A	369	-11.953	55.158	26.287	1.00	32.03
ATOM	1216	O	TYR	A	369	-10.842	55.634	26.529	1.00	28.95
ATOM	1217	N	TYR	A	370	-12.996	55.828	25.851	1.00	32.03
ATOM	1218	OH	TYR	A	370	-13.216	63.382	23.761	1.00	38.96
ATOM	1219	CD2	TYR	A	370	-14.752	60.205	24.698	1.00	36.28
ATOM	1220	CE2	TYR	A	370	-14.597	61.568	24.490	1.00	36.78
ATOM	1221	CZ	TYR	A	370	-13.409	62.034	23.975	1.00	37.70
ATOM	1222	CE1	TYR	A	370	-12.383	61.168	23.662	1.00	36.85
ATOM	1223	CD1	TYR	A	370	-12.563	59.820	23.871	1.00	35.73
ATOM	1224	CG	TYR	A	370	-13.741	59.312	24.388	1.00	35.35
ATOM	1225	CB	TYR	A	370	-13.896	57.816	24.613	1.00	34.74
ATOM	1226	CA	TYR	A	370	-12.850	57.254	25.574	1.00	33.23
ATOM	1227	C	TYR	A	370	-12.982	57.999	26.897	1.00	33.56
ATOM	1228	O	TYR	A	370	-13.819	57.580	27.684	1.00	33.28
ATOM	1229	N	SER	A	371	-12.169	59.015	27.125	1.00	35.61

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1230	OG	SER	A	371	-10.952	60.534	30.263	1.00	37.79
ATOM	1231	CB	SER	A	371	-10.994	59.623	29.183	1.00	39.02
ATOM	1232	CA	SER	A	371	-12.297	59.726	28.389	1.00	38.04
ATOM	1233	C	SER	A	371	-12.666	61.187	28.201	1.00	39.91
ATOM	1234	O	SER	A	371	-11.843	62.022	27.853	1.00	38.57
ATOM	1235	N	PRO	A	372	-13.931	61.484	28.420	1.00	43.18
ATOM	1236	CG	PRO	A	372	-16.243	61.324	28.452	1.00	44.76
ATOM	1237	CD	PRO	A	372	-15.008	60.574	28.867	1.00	44.03
ATOM	1238	CB	PRO	A	372	-15.900	62.772	28.425	1.00	45.09
ATOM	1239	CA	PRO	A	372	-14.403	62.878	28.437	1.00	45.43
ATOM	1240	C	PRO	A	372	-13.833	63.366	29.760	1.00	46.59
ATOM	1241	O	PRO	A	372	-14.102	62.743	30.789	1.00	47.64
ATOM	1242	N	VAL	A	373	-12.978	64.362	29.767	1.00	48.18
ATOM	1243	CG2	VAL	A	373	-13.693	65.070	32.937	1.00	48.74
ATOM	1244	CG1	VAL	A	373	-11.354	64.454	33.270	1.00	48.15
ATOM	1245	CB	VAL	A	373	-12.534	64.295	32.314	1.00	48.02
ATOM	1246	CA	VAL	A	373	-12.176	64.754	30.916	1.00	47.53
ATOM	1247	C	VAL	A	373	-10.843	64.081	30.527	1.00	47.84
ATOM	1248	O	VAL	A	373	-10.706	62.871	30.685	1.00	48.07
ATOM	1249	N	GLY	A	374	-9.966	64.870	29.936	1.00	46.71
ATOM	1250	CA	GLY	A	374	-8.687	64.329	29.474	1.00	45.92
ATOM	1251	C	GLY	A	374	-8.718	64.327	27.946	1.00	44.34
ATOM	1252	O	GLY	A	374	-7.703	64.386	27.276	1.00	43.53
ATOM	1253	N	LYS	A	375	-9.937	64.227	27.433	1.00	20.00
ATOM	1254	NZ	LYS	A	375	-11.621	70.469	25.481	1.00	20.00
ATOM	1255	CE	LYS	A	375	-11.822	69.108	25.996	1.00	20.00
ATOM	1256	CD	LYS	A	375	-10.786	68.111	25.474	1.00	20.00
ATOM	1257	CG	LYS	A	375	-10.999	66.697	26.013	1.00	20.00
ATOM	1258	CB	LYS	A	375	-9.976	65.697	25.486	1.00	20.00
ATOM	1259	CA	LYS	A	375	-10.201	64.262	26.011	1.00	20.00
ATOM	1260	C	LYS	A	375	-9.308	63.297	25.260	1.00	20.00
ATOM	1261	O	LYS	A	375	-8.529	63.725	24.411	1.00	20.00
ATOM	1262	N	LYS	A	376	-9.386	62.003	25.604	1.00	20.00
ATOM	1263	NZ	LYS	A	376	-3.285	64.692	24.559	1.00	20.00
ATOM	1264	CE	LYS	A	376	-4.696	64.381	24.290	1.00	20.00
ATOM	1265	CD	LYS	A	376	-5.139	63.045	24.890	1.00	20.00
ATOM	1266	CG	LYS	A	376	-6.606	62.726	24.608	1.00	20.00
ATOM	1267	CB	LYS	A	376	-7.050	61.390	25.194	1.00	20.00
ATOM	1268	CA	LYS	A	376	-8.531	61.050	24.897	1.00	20.00
ATOM	1269	C	LYS	A	376	-8.810	59.601	25.286	1.00	20.00
ATOM	1270	O	LYS	A	376	-9.696	59.281	26.077	1.00	20.00
ATOM	1271	N	ASN	A	377	-8.050	58.726	24.640	1.00	29.74
ATOM	1272	CA	ASN	A	377	-8.240	57.295	24.862	1.00	29.33
ATOM	1273	CB	ASN	A	377	-7.825	56.539	23.612	1.00	29.66
ATOM	1274	CG	ASN	A	377	-8.743	56.803	22.433	1.00	30.76
ATOM	1275	OD1	ASN	A	377	-9.964	56.948	22.559	1.00	29.66
ATOM	1276	ND2	ASN	A	377	-8.128	56.865	21.249	1.00	31.26
ATOM	1277	C	ASN	A	377	-7.486	56.848	26.098	1.00	28.35
ATOM	1278	O	ASN	A	377	-6.411	57.376	26.306	1.00	26.83
ATOM	1279	N	ILE	A	378	-8.123	56.055	26.952	1.00	26.88
ATOM	1280	CA	ILE	A	378	-7.431	55.408	28.039	1.00	28.08
ATOM	1281	CB	ILE	A	378	-7.802	55.780	29.473	1.00	29.37
ATOM	1282	CG2	ILE	A	378	-7.624	57.282	29.706	1.00	28.66
ATOM	1283	CG1	ILE	A	378	-9.217	55.317	29.789	1.00	31.06

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1284	CD1	ILE	A	378	-9.563	55.301	31.261	1.00	32.92
ATOM	1285	C	ILE	A	378	-7.567	53.887	27.882	1.00	26.65
ATOM	1286	O	ILE	A	378	-8.559	53.283	27.479	1.00	25.21
ATOM	1287	N	TYR	A	379	-6.456	53.246	28.250	1.00	25.14
ATOM	1288	CA	TYR	A	379	-6.298	51.805	28.141	1.00	23.62
ATOM	1289	CB	TYR	A	379	-5.057	51.473	27.299	1.00	25.30
ATOM	1290	CG	TYR	A	379	-5.076	52.202	25.979	1.00	27.60
ATOM	1291	CD1	TYR	A	379	-4.644	53.523	25.919	1.00	28.62
ATOM	1292	CE1	TYR	A	379	-4.683	54.224	24.736	1.00	30.42
ATOM	1293	CD2	TYR	A	379	-5.571	51.619	24.836	1.00	28.58
ATOM	1294	CE2	TYR	A	379	-5.582	52.298	23.634	1.00	29.43
ATOM	1295	CZ	TYR	A	379	-5.141	53.597	23.603	1.00	30.50
ATOM	1296	OH	TYR	A	379	-5.162	54.325	22.441	1.00	33.44
ATOM	1297	C	TYR	A	379	-6.141	51.154	29.498	1.00	22.07
ATOM	1298	O	TYR	A	379	-5.164	51.460	30.204	1.00	22.84
ATOM	1299	N	LEU	A	380	-6.941	50.122	29.768	1.00	16.20
ATOM	1300	CA	LEU	A	380	-6.831	49.396	30.998	1.00	17.68
ATOM	1301	CB	LEU	A	380	-8.233	49.019	31.490	1.00	19.14
ATOM	1302	CG	LEU	A	380	-9.204	50.207	31.624	1.00	21.74
ATOM	1303	CD1	LEU	A	380	-10.479	49.690	32.285	1.00	22.06
ATOM	1304	CD2	LEU	A	380	-8.614	51.364	32.411	1.00	20.08
ATOM	1305	C	LEU	A	380	-5.903	48.191	30.845	1.00	13.92
ATOM	1306	O	LEU	A	380	-6.249	47.139	31.351	1.00	12.26
ATOM	1307	N	ASN	A	381	-4.762	48.385	30.190	1.00	14.40
ATOM	1308	CA	ASN	A	381	-3.798	47.282	30.009	1.00	15.71
ATOM	1309	CB	ASN	A	381	-3.148	47.364	28.646	1.00	13.12
ATOM	1310	CG	ASN	A	381	-2.442	48.681	28.373	1.00	13.93
ATOM	1311	OD1	ASN	A	381	-2.614	49.693	29.057	1.00	15.98
ATOM	1312	ND2	ASN	A	381	-1.584	48.766	27.386	1.00	13.77
ATOM	1313	C	ASN	A	381	-2.732	47.428	31.111	1.00	15.34
ATOM	1314	O	ASN	A	381	-1.538	47.496	30.826	1.00	19.25
ATOM	1315	N	SER	A	382	-3.178	47.587	32.318	1.00	14.28
ATOM	1316	CA	SER	A	382	-2.363	47.953	33.462	1.00	16.49
ATOM	1317	CB	SER	A	382	-2.722	49.449	33.712	1.00	19.36
ATOM	1318	OG	SER	A	382	-4.021	49.622	34.261	1.00	19.22
ATOM	1319	C	SER	A	382	-2.534	47.168	34.720	1.00	13.50
ATOM	1320	O	SER	A	382	-3.491	46.443	34.986	1.00	14.79
ATOM	1321	N	GLY	A	383	-1.543	47.226	35.602	1.00	12.08
ATOM	1322	CA	GLY	A	383	-1.460	46.552	36.865	1.00	7.68
ATOM	1323	C	GLY	A	383	-0.407	47.250	37.737	1.00	9.13
ATOM	1324	O	GLY	A	383	0.356	48.018	37.167	1.00	7.23
ATOM	1325	N	LEU	A	384	-0.406	46.961	39.018	1.00	9.60
ATOM	1326	CA	LEU	A	384	0.596	47.604	39.860	1.00	10.98
ATOM	1327	CB	LEU	A	384	0.108	48.911	40.437	1.00	10.87
ATOM	1328	CG	LEU	A	384	-1.098	48.840	41.372	1.00	12.55
ATOM	1329	CD1	LEU	A	384	-0.751	48.583	42.819	1.00	11.84
ATOM	1330	CD2	LEU	A	384	-1.824	50.197	41.305	1.00	14.27
ATOM	1331	C	LEU	A	384	0.963	46.614	40.982	1.00	11.40
ATOM	1332	O	LEU	A	384	0.191	45.705	41.269	1.00	12.17
ATOM	1333	N	THR	A	385	2.174	46.774	41.470	1.00	10.30
ATOM	1334	CA	THR	A	385	2.773	45.977	42.535	1.00	10.05
ATOM	1335	CB	THR	A	385	3.958	45.170	41.969	1.00	11.82
ATOM	1336	OG1	THR	A	385	3.463	44.161	41.100	1.00	12.53
ATOM	1337	CG2	THR	A	385	4.842	44.430	42.991	1.00	7.93

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1338	C	THR	A	385	3.429	46.936	43.546	1.00	10.37
ATOM	1339	O	THR	A	385	4.154	47.869	43.150	1.00	10.04
ATOM	1340	N	SER	A	386	3.153	46.751	44.806	1.00	10.16
ATOM	1341	CA	SER	A	386	3.835	47.470	45.853	1.00	12.08
ATOM	1342	CB	SER	A	386	2.913	47.978	46.925	1.00	12.65
ATOM	1343	OG	SER	A	386	3.625	48.590	47.976	1.00	12.90
ATOM	1344	C	SER	A	386	4.773	46.445	46.540	1.00	11.71
ATOM	1345	O	SER	A	386	4.348	45.314	46.714	1.00	11.70
ATOM	1346	N	THR	A	387	5.929	46.899	46.978	1.00	13.21
ATOM	1347	CA	THR	A	387	6.861	46.004	47.677	1.00	11.54
ATOM	1348	CB	THR	A	387	8.258	45.976	47.083	1.00	12.46
ATOM	1349	OG1	THR	A	387	8.794	47.305	46.902	1.00	12.52
ATOM	1350	CG2	THR	A	387	8.193	45.224	45.771	1.00	9.84
ATOM	1351	C	THR	A	387	6.917	46.429	49.137	1.00	12.59
ATOM	1352	O	THR	A	387	7.750	45.916	49.857	1.00	9.86
ATOM	1353	N	LYS	A	388	5.888	47.176	49.559	1.00	10.11
ATOM	1354	CA	LYS	A	388	5.781	47.451	50.983	1.00	11.18
ATOM	1355	CB	LYS	A	388	5.844	48.928	51.315	1.00	10.27
ATOM	1356	CG	LYS	A	388	5.598	49.163	52.809	1.00	11.78
ATOM	1357	CD	LYS	A	388	5.570	50.665	53.086	1.00	12.59
ATOM	1358	CE	LYS	A	388	5.610	50.846	54.616	1.00	12.42
ATOM	1359	NZ	LYS	A	388	5.400	52.289	54.915	1.00	12.86
ATOM	1360	C	LYS	A	388	4.466	46.836	51.470	1.00	12.79
ATOM	1361	O	LYS	A	388	3.445	47.068	50.803	1.00	13.47
ATOM	1362	N	ASN	A	389	4.490	46.117	52.561	1.00	11.20
ATOM	1363	CA	ASN	A	389	3.235	45.595	53.114	1.00	13.05
ATOM	1364	CB	ASN	A	389	2.797	44.247	52.498	1.00	9.98
ATOM	1365	CG	ASN	A	389	1.328	43.929	52.695	1.00	13.57
ATOM	1366	OD1	ASN	A	389	0.562	44.823	53.020	1.00	11.41
ATOM	1367	ND2	ASN	A	389	0.828	42.697	52.544	1.00	11.87
ATOM	1368	C	ASN	A	389	3.401	45.431	54.605	1.00	12.01
ATOM	1369	O	ASN	A	389	4.389	44.832	55.045	1.00	12.68
ATOM	1370	N	TYR	A	390	2.463	45.891	55.415	1.00	9.33
ATOM	1371	CA	TYR	A	390	2.544	45.725	56.834	1.00	11.32
ATOM	1372	CB	TYR	A	390	2.395	44.317	57.360	1.00	13.01
ATOM	1373	CG	TYR	A	390	1.034	43.646	57.138	1.00	17.63
ATOM	1374	CD1	TYR	A	390	0.888	42.699	56.135	1.00	17.99
ATOM	1375	CE1	TYR	A	390	-0.324	42.059	55.906	1.00	18.34
ATOM	1376	CD2	TYR	A	390	-0.059	43.950	57.918	1.00	17.56
ATOM	1377	CE2	TYR	A	390	-1.295	43.344	57.684	1.00	19.81
ATOM	1378	CZ	TYR	A	390	-1.408	42.399	56.685	1.00	18.72
ATOM	1379	OH	TYR	A	390	-2.599	41.770	56.456	1.00	18.16
ATOM	1380	C	TYR	A	390	3.875	46.390	57.342	1.00	11.32
ATOM	1381	O	TYR	A	390	4.444	45.867	58.262	1.00	10.06
ATOM	1382	N	GLY	A	391	4.202	47.568	56.849	1.00	12.38
ATOM	1383	CA	GLY	A	391	5.264	48.396	57.395	1.00	13.46
ATOM	1384	C	GLY	A	391	6.671	47.822	57.226	1.00	14.75
ATOM	1385	O	GLY	A	391	7.615	48.218	57.920	1.00	13.47
ATOM	1386	N	LYS	A	392	6.864	47.001	56.213	1.00	14.18
ATOM	1387	NZ	LYS	A	392	6.391	42.087	59.901	1.00	31.24
ATOM	1388	CE	LYS	A	392	6.545	43.004	58.726	1.00	30.06
ATOM	1389	CD	LYS	A	392	7.980	43.237	58.298	1.00	27.75
ATOM	1390	CG	LYS	A	392	8.231	44.701	57.942	1.00	25.41
ATOM	1391	CB	LYS	A	392	8.133	44.929	56.460	1.00	20.56

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1392	CA	LYS	A	392	8.133	46.376	55.909	1.00	15.94
ATOM	1393	C	LYS	A	392	8.265	46.221	54.399	1.00	14.65
ATOM	1394	O	LYS	A	392	7.242	46.070	53.676	1.00	12.21
ATOM	1395	N	THR	A	393	9.481	45.969	53.965	1.00	9.88
ATOM	1396	CA	THR	A	393	9.744	45.629	52.574	1.00	10.28
ATOM	1397	CB	THR	A	393	11.178	45.988	52.155	1.00	10.31
ATOM	1398	OG1	THR	A	393	11.412	47.397	52.330	1.00	9.91
ATOM	1399	CG2	THR	A	393	11.393	45.631	50.693	1.00	7.83
ATOM	1400	C	THR	A	393	9.450	44.139	52.450	1.00	11.39
ATOM	1401	O	THR	A	393	9.872	43.332	53.278	1.00	11.16
ATOM	1402	N	ILE	A	394	8.715	43.737	51.398	1.00	8.47
ATOM	1403	CA	ILE	A	394	8.413	42.305	51.297	1.00	8.59
ATOM	1404	CB	ILE	A	394	7.223	42.076	50.329	1.00	7.43
ATOM	1405	CG2	ILE	A	394	6.044	42.929	50.867	1.00	5.89
ATOM	1406	CG1	ILE	A	394	7.562	42.401	48.910	1.00	7.72
ATOM	1407	CD1	ILE	A	394	6.413	42.268	47.877	1.00	9.17
ATOM	1408	C	ILE	A	394	9.657	41.573	50.761	1.00	9.33
ATOM	1409	O	ILE	A	394	10.482	42.262	50.170	1.00	8.55
ATOM	1410	N	LEU	A	395	9.689	40.276	50.913	1.00	7.97
ATOM	1411	CA	LEU	A	395	10.808	39.499	50.347	1.00	11.81
ATOM	1412	CB	LEU	A	395	10.545	37.998	50.620	1.00	12.21
ATOM	1413	CG	LEU	A	395	10.370	37.651	52.090	1.00	13.09
ATOM	1414	CD1	LEU	A	395	10.246	36.140	52.313	1.00	10.90
ATOM	1415	CD2	LEU	A	395	11.569	38.245	52.832	1.00	13.70
ATOM	1416	C	LEU	A	395	10.920	39.603	48.860	1.00	13.57
ATOM	1417	O	LEU	A	395	9.864	39.692	48.193	1.00	11.36
ATOM	1418	N	THR	A	396	12.089	39.426	48.281	1.00	9.31
ATOM	1419	CA	THR	A	396	12.273	39.345	46.840	1.00	11.95
ATOM	1420	CB	THR	A	396	13.746	39.021	46.476	1.00	14.52
ATOM	1421	OG1	THR	A	396	14.575	40.034	47.090	1.00	16.31
ATOM	1422	CG2	THR	A	396	13.983	39.148	44.996	1.00	16.49
ATOM	1423	C	THR	A	396	11.376	38.264	46.209	1.00	12.19
ATOM	1424	O	THR	A	396	10.790	38.544	45.152	1.00	11.09
ATOM	1425	N	LYS	A	397	11.286	37.104	46.840	1.00	9.73
ATOM	1426	CA	LYS	A	397	10.451	36.033	46.298	1.00	12.22
ATOM	1427	CB	LYS	A	397	10.630	34.680	46.935	1.00	11.19
ATOM	1428	CG	LYS	A	397	10.365	34.491	48.402	1.00	10.22
ATOM	1429	CD	LYS	A	397	10.459	32.971	48.678	1.00	12.87
ATOM	1430	CE	LYS	A	397	9.904	32.634	50.049	1.00	10.59
ATOM	1431	NZ	LYS	A	397	10.430	31.409	50.690	1.00	13.72
ATOM	1432	C	LYS	A	397	8.946	36.390	46.379	1.00	11.16
ATOM	1433	O	LYS	A	397	8.250	35.937	45.488	1.00	10.09
ATOM	1434	N	GLU	A	398	8.588	37.196	47.346	1.00	10.22
ATOM	1435	CA	GLU	A	398	7.207	37.628	47.475	1.00	13.12
ATOM	1436	CB	GLU	A	398	6.931	38.233	48.857	1.00	11.64
ATOM	1437	CG	GLU	A	398	6.951	37.079	49.876	1.00	15.45
ATOM	1438	CD	GLU	A	398	6.952	37.662	51.284	1.00	15.72
ATOM	1439	OE1	GLU	A	398	7.139	38.861	51.557	1.00	15.77
ATOM	1440	OE2	GLU	A	398	6.722	36.861	52.186	1.00	17.81
ATOM	1441	C	GLU	A	398	6.875	38.628	46.374	1.00	14.23
ATOM	1442	O	GLU	A	398	5.819	38.496	45.746	1.00	11.36
ATOM	1443	N	ALA	A	399	7.791	39.566	46.144	1.00	11.71
ATOM	1444	CA	ALA	A	399	7.603	40.571	45.121	1.00	10.93
ATOM	1445	CB	ALA	A	399	8.705	41.611	45.021	1.00	10.46

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1446	C	ALA	A	399	7.464	39.901	43.737	1.00	11.66
ATOM	1447	O	ALA	A	399	6.535	40.310	43.047	1.00	8.52
ATOM	1448	N	ASP	A	400	8.259	38.892	43.411	1.00	10.58
ATOM	1449	CA	ASP	A	400	8.092	38.172	42.164	1.00	11.27
ATOM	1450	CB	ASP	A	400	9.061	37.001	41.994	1.00	13.33
ATOM	1451	CG	ASP	A	400	10.525	37.443	41.936	1.00	15.25
ATOM	1452	OD1	ASP	A	400	10.787	38.685	41.868	1.00	11.52
ATOM	1453	OD2	ASP	A	400	11.331	36.459	41.963	1.00	15.55
ATOM	1454	C	ASP	A	400	6.682	37.543	42.061	1.00	10.74
ATOM	1455	O	ASP	A	400	6.102	37.681	40.959	1.00	11.54
ATOM	1456	N	LEU	A	401	6.184	37.034	43.155	1.00	9.91
ATOM	1457	CA	LEU	A	401	4.860	36.399	43.132	1.00	12.48
ATOM	1458	CB	LEU	A	401	4.618	35.610	44.411	1.00	13.67
ATOM	1459	CG	LEU	A	401	5.551	34.464	44.805	1.00	19.11
ATOM	1460	CD1	LEU	A	401	5.596	34.451	46.337	1.00	20.83
ATOM	1461	CD2	LEU	A	401	5.072	33.125	44.302	1.00	19.44
ATOM	1462	C	LEU	A	401	3.724	37.434	42.994	1.00	11.96
ATOM	1463	O	LEU	A	401	2.701	37.092	42.388	1.00	9.62
ATOM	1464	N	VAL	A	402	3.849	38.626	43.576	1.00	9.23
ATOM	1465	CA	VAL	A	402	2.856	39.664	43.347	1.00	10.16
ATOM	1466	CB	VAL	A	402	3.222	40.976	44.086	1.00	11.53
ATOM	1467	CG1	VAL	A	402	2.219	42.096	43.805	1.00	10.53
ATOM	1468	CG2	VAL	A	402	3.254	40.598	45.565	1.00	8.46
ATOM	1469	C	VAL	A	402	2.701	40.016	41.882	1.00	12.23
ATOM	1470	O	VAL	A	402	1.581	40.096	41.336	1.00	9.50
ATOM	1471	N	THR	A	403	3.821	40.359	41.261	1.00	8.92
ATOM	1472	CA	THR	A	403	3.845	40.764	39.883	1.00	8.22
ATOM	1473	CB	THR	A	403	5.220	41.259	39.386	1.00	6.99
ATOM	1474	OG1	THR	A	403	5.612	42.325	40.255	1.00	6.97
ATOM	1475	CG2	THR	A	403	5.221	41.841	37.998	1.00	6.87
ATOM	1476	C	THR	A	403	3.381	39.610	38.992	1.00	9.35
ATOM	1477	O	THR	A	403	2.693	39.954	38.016	1.00	5.99
ATOM	1478	N	THR	A	404	3.855	38.407	39.301	1.00	6.34
ATOM	1479	CA	THR	A	404	3.382	37.249	38.521	1.00	7.96
ATOM	1480	CB	THR	A	404	3.962	35.946	39.104	1.00	8.71
ATOM	1481	OG1	THR	A	404	5.404	35.959	38.945	1.00	8.46
ATOM	1482	CG2	THR	A	404	3.448	34.743	38.303	1.00	8.11
ATOM	1483	C	THR	A	404	1.842	37.175	38.572	1.00	6.99
ATOM	1484	O	THR	A	404	1.211	36.979	37.529	1.00	6.33
ATOM	1485	N	HIS	A	405	1.298	37.277	39.751	1.00	6.76
ATOM	1486	CA	HIS	A	405	-0.132	37.232	40.003	1.00	9.62
ATOM	1487	CB	HIS	A	405	-0.383	37.343	41.495	1.00	7.56
ATOM	1488	CG	HIS	A	405	-1.828	37.311	41.919	1.00	6.65
ATOM	1489	CD2	HIS	A	405	-2.801	38.292	41.862	1.00	4.31
ATOM	1490	ND1	HIS	A	405	-2.389	36.204	42.467	1.00	7.16
ATOM	1491	CE1	HIS	A	405	-3.664	36.486	42.798	1.00	9.20
ATOM	1492	NE2	HIS	A	405	-3.937	37.722	42.413	1.00	9.52
ATOM	1493	C	HIS	A	405	-0.867	38.376	39.290	1.00	9.96
ATOM	1494	O	HIS	A	405	-1.836	38.080	38.597	1.00	9.05
ATOM	1495	N	GLU	A	406	-0.414	39.612	39.416	1.00	9.09
ATOM	1496	CA	GLU	A	406	-1.106	40.730	38.755	1.00	11.72
ATOM	1497	CB	GLU	A	406	-0.532	42.078	39.207	1.00	12.02
ATOM	1498	CG	GLU	A	406	-0.582	42.239	40.701	1.00	11.63
ATOM	1499	CD	GLU	A	406	-1.940	42.013	41.321	1.00	12.61

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1500	OE1	GLU	A	406	-2.985	42.048	40.632	1.00	12.02
ATOM	1501	OE2	GLU	A	406	-1.910	41.759	42.535	1.00	12.54
ATOM	1502	C	GLU	A	406	-1.087	40.659	37.256	1.00	13.24
ATOM	1503	O	GLU	A	406	-2.110	40.827	36.529	1.00	10.09
ATOM	1504	N	LEU	A	407	0.115	40.341	36.745	1.00	9.35
ATOM	1505	CA	LEU	A	407	0.259	40.106	35.318	1.00	11.31
ATOM	1506	CB	LEU	A	407	1.702	39.802	34.937	1.00	13.34
ATOM	1507	CG	LEU	A	407	2.671	40.844	34.384	1.00	17.06
ATOM	1508	CD1	LEU	A	407	2.232	42.279	34.412	1.00	15.35
ATOM	1509	CD2	LEU	A	407	4.112	40.690	34.878	1.00	15.89
ATOM	1510	C	LEU	A	407	-0.675	38.971	34.886	1.00	8.96
ATOM	1511	O	LEU	A	407	-1.105	38.869	33.720	1.00	9.09
ATOM	1512	N	GLY	A	408	-0.837	37.972	35.732	1.00	7.26
ATOM	1513	CA	GLY	A	408	-1.649	36.774	35.444	1.00	7.95
ATOM	1514	C	GLY	A	408	-3.107	37.247	35.182	1.00	8.27
ATOM	1515	O	GLY	A	408	-3.776	36.757	34.277	1.00	7.64
ATOM	1516	N	HIS	A	409	-3.565	38.171	36.030	1.00	10.19
ATOM	1517	CA	HIS	A	409	-4.873	38.777	35.752	1.00	11.21
ATOM	1518	CB	HIS	A	409	-5.162	39.920	36.713	1.00	8.68
ATOM	1519	CG	HIS	A	409	-5.605	39.404	38.018	1.00	10.30
ATOM	1520	CD2	HIS	A	409	-5.193	39.710	39.255	1.00	9.44
ATOM	1521	ND1	HIS	A	409	-6.606	38.454	38.114	1.00	10.06
ATOM	1522	CE1	HIS	A	409	-6.833	38.237	39.402	1.00	12.63
ATOM	1523	NE2	HIS	A	409	-5.961	38.972	40.132	1.00	12.50
ATOM	1524	C	HIS	A	409	-4.918	39.414	34.381	1.00	12.04
ATOM	1525	O	HIS	A	409	-5.853	39.223	33.615	1.00	12.02
ATOM	1526	N	ASN	A	410	-3.910	40.235	34.085	1.00	11.36
ATOM	1527	CA	ASN	A	410	-3.859	40.925	32.820	1.00	10.24
ATOM	1528	CB	ASN	A	410	-2.594	41.750	32.616	1.00	10.71
ATOM	1529	CG	ASN	A	410	-2.499	43.027	33.424	1.00	12.40
ATOM	1530	OD1	ASN	A	410	-1.369	43.394	33.748	1.00	9.72
ATOM	1531	ND2	ASN	A	410	-3.598	43.762	33.714	1.00	9.17
ATOM	1532	C	ASN	A	410	-3.953	39.918	31.675	1.00	12.78
ATOM	1533	O	ASN	A	410	-4.538	40.276	30.652	1.00	9.40
ATOM	1534	N	PHE	A	411	-3.292	38.782	31.796	1.00	9.09
ATOM	1535	CA	PHE	A	411	-3.280	37.693	30.872	1.00	10.91
ATOM	1536	CB	PHE	A	411	-2.105	36.703	31.101	1.00	10.93
ATOM	1537	CG	PHE	A	411	-0.840	37.086	30.375	1.00	13.69
ATOM	1538	CD1	PHE	A	411	-0.102	38.216	30.730	1.00	15.12
ATOM	1539	CD2	PHE	A	411	-0.309	36.297	29.389	1.00	15.69
ATOM	1540	CE1	PHE	A	411	1.076	38.546	30.052	1.00	13.51
ATOM	1541	CE2	PHE	A	411	0.862	36.617	28.723	1.00	15.64
ATOM	1542	CZ	PHE	A	411	1.556	37.782	29.051	1.00	14.11
ATOM	1543	C	PHE	A	411	-4.606	36.903	30.849	1.00	10.27
ATOM	1544	O	PHE	A	411	-4.684	36.100	29.931	1.00	9.02
ATOM	1545	N	GLY	A	412	-5.578	37.150	31.701	1.00	11.88
ATOM	1546	CA	GLY	A	412	-6.912	36.517	31.563	1.00	11.02
ATOM	1547	C	GLY	A	412	-7.360	35.734	32.748	1.00	12.85
ATOM	1548	O	GLY	A	412	-8.496	35.256	32.898	1.00	11.80
ATOM	1549	N	ALA	A	413	-6.418	35.577	33.737	1.00	9.39
ATOM	1550	CA	ALA	A	413	-6.759	34.738	34.860	1.00	8.60
ATOM	1551	CB	ALA	A	413	-5.523	34.078	35.504	1.00	6.06
ATOM	1552	C	ALA	A	413	-7.520	35.451	35.966	1.00	9.94
ATOM	1553	O	ALA	A	413	-7.216	36.584	36.300	1.00	9.19

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1554	N	GLU	A	414	-8.476	34.694	36.530	1.00	9.61
ATOM	1555	CA	GLU	A	414	-9.172	35.158	37.731	1.00	12.27
ATOM	1556	CB	GLU	A	414	-10.666	34.812	37.677	1.00	14.74
ATOM	1557	CG	GLU	A	414	-11.293	35.591	36.517	1.00	16.17
ATOM	1558	CD	GLU	A	414	-11.696	36.987	36.834	1.00	20.61
ATOM	1559	OE1	GLU	A	414	-11.520	37.544	37.933	1.00	21.11
ATOM	1560	OE2	GLU	A	414	-12.266	37.646	35.920	1.00	24.06
ATOM	1561	C	GLU	A	414	-8.509	34.457	38.920	1.00	12.40
ATOM	1562	O	GLU	A	414	-7.455	33.841	38.757	1.00	12.29
ATOM	1563	N	HIS	A	415	-9.108	34.478	40.104	1.00	11.96
ATOM	1564	CA	HIS	A	415	-8.512	33.849	41.259	1.00	13.28
ATOM	1565	CB	HIS	A	415	-9.093	34.484	42.514	1.00	12.84
ATOM	1566	CG	HIS	A	415	-8.513	35.841	42.716	1.00	11.55
ATOM	1567	CD2	HIS	A	415	-7.240	36.265	42.433	1.00	11.21
ATOM	1568	ND1	HIS	A	415	-9.180	36.899	43.276	1.00	10.77
ATOM	1569	CE1	HIS	A	415	-8.380	37.944	43.314	1.00	9.60
ATOM	1570	NE2	HIS	A	415	-7.174	37.576	42.791	1.00	11.71
ATOM	1571	C	HIS	A	415	-8.789	32.362	41.293	1.00	14.34
ATOM	1572	O	HIS	A	415	-9.851	32.007	40.751	1.00	10.53
ATOM	1573	N	ASP	A	416	-7.855	31.567	41.826	1.00	10.07
ATOM	1574	CA	ASP	A	416	-8.239	30.158	41.962	1.00	11.05
ATOM	1575	CB	ASP	A	416	-6.978	29.338	42.310	1.00	13.78
ATOM	1576	CG	ASP	A	416	-5.913	29.387	41.229	1.00	14.67
ATOM	1577	OD1	ASP	A	416	-6.267	29.373	40.039	1.00	13.81
ATOM	1578	OD2	ASP	A	416	-4.717	29.403	41.608	1.00	16.01
ATOM	1579	C	ASP	A	416	-9.254	29.930	43.052	1.00	10.40
ATOM	1580	O	ASP	A	416	-9.169	30.468	44.159	1.00	11.17
ATOM	1581	N	PRO	A	417	-10.296	29.111	42.805	1.00	10.30
ATOM	1582	CD	PRO	A	417	-10.544	28.473	41.502	1.00	12.83
ATOM	1583	CA	PRO	A	417	-11.275	28.774	43.805	1.00	12.54
ATOM	1584	CB	PRO	A	417	-12.495	28.328	42.975	1.00	13.91
ATOM	1585	CG	PRO	A	417	-11.940	27.894	41.674	1.00	15.31
ATOM	1586	C	PRO	A	417	-10.837	27.603	44.689	1.00	13.42
ATOM	1587	O	PRO	A	417	-10.002	26.839	44.276	1.00	14.77
ATOM	1588	N	ASP	A	418	-11.346	27.376	45.860	1.00	14.02
ATOM	1589	CA	ASP	A	418	-11.086	26.217	46.694	1.00	20.43
ATOM	1590	CB	ASP	A	418	-11.375	26.531	48.172	1.00	22.42
ATOM	1591	CG	ASP	A	418	-10.416	27.595	48.658	1.00	25.60
ATOM	1592	OD1	ASP	A	418	-9.221	27.416	48.429	1.00	27.33
ATOM	1593	OD2	ASP	A	418	-10.724	28.666	49.204	1.00	29.81
ATOM	1594	C	ASP	A	418	-11.997	25.061	46.257	1.00	23.39
ATOM	1595	O	ASP	A	418	-13.034	25.354	45.640	1.00	23.78
ATOM	1596	N	GLY	A	419	-11.533	23.829	46.307	1.00	24.01
ATOM	1597	CA	GLY	A	419	-12.290	22.650	46.050	1.00	28.51
ATOM	1598	C	GLY	A	419	-12.000	21.714	44.916	1.00	31.09
ATOM	1599	O	GLY	A	419	-11.000	21.726	44.169	1.00	31.19
ATOM	1600	N	LEU	A	420	-12.976	20.849	44.625	1.00	32.09
ATOM	1601	CD2	LEU	A	420	-14.406	17.142	44.111	1.00	38.06
ATOM	1602	CD1	LEU	A	420	-16.571	18.444	44.050	1.00	37.27
ATOM	1603	CG	LEU	A	420	-15.061	18.507	44.238	1.00	36.91
ATOM	1604	CB	LEU	A	420	-14.424	19.470	43.224	1.00	36.82
ATOM	1605	CA	LEU	A	420	-12.969	19.843	43.591	1.00	35.26
ATOM	1606	C	LEU	A	420	-12.193	20.130	42.331	1.00	36.08
ATOM	1607	O	LEU	A	420	-11.638	19.221	41.701	1.00	37.02

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1608	N	ALA	A	421	-12.053	21.380	41.907	1.00	36.27
ATOM	1609	CB	ALA	A	421	-11.478	23.254	40.472	1.00	37.17
ATOM	1610	CA	ALA	A	421	-11.309	21.755	40.742	1.00	36.49
ATOM	1611	C	ALA	A	421	-9.841	21.381	40.794	1.00	35.18
ATOM	1612	O	ALA	A	421	-9.253	21.402	39.702	1.00	36.10
ATOM	1613	N	GLU	A	422	-9.183	21.102	41.907	1.00	32.65
ATOM	1614	OE2	GLU	A	422	-8.104	20.106	37.709	1.00	41.16
ATOM	1615	OE1	GLU	A	422	-6.137	19.284	37.500	1.00	39.97
ATOM	1616	CD	GLU	A	422	-6.983	19.889	38.198	1.00	38.24
ATOM	1617	CG	GLU	A	422	-6.628	20.311	39.582	1.00	35.89
ATOM	1618	CB	GLU	A	422	-7.426	19.813	40.760	1.00	31.03
ATOM	1619	CA	GLU	A	422	-7.761	20.769	41.914	1.00	29.38
ATOM	1620	C	GLU	A	422	-6.901	22.028	41.779	1.00	24.25
ATOM	1621	O	GLU	A	422	-5.677	21.951	41.645	1.00	21.69
ATOM	1622	N	CYS	A	423	-7.530	23.185	41.837	1.00	19.59
ATOM	1623	CA	CYS	A	423	-6.862	24.457	41.613	1.00	18.31
ATOM	1624	CB	CYS	A	423	-7.819	25.319	40.797	1.00	21.54
ATOM	1625	SG	CYS	A	423	-8.112	24.725	39.090	1.00	22.74
ATOM	1626	C	CYS	A	423	-6.367	25.102	42.893	1.00	16.82
ATOM	1627	O	CYS	A	423	-5.884	26.233	42.855	1.00	14.86
ATOM	1628	N	ALA	A	424	-6.516	24.451	44.029	1.00	15.16
ATOM	1629	CA	ALA	A	424	-5.974	24.991	45.288	1.00	16.52
ATOM	1630	CB	ALA	A	424	-6.940	25.972	45.924	1.00	15.07
ATOM	1631	C	ALA	A	424	-5.603	23.812	46.165	1.00	15.42
ATOM	1632	O	ALA	A	424	-6.206	23.507	47.182	1.00	16.31
ATOM	1633	N	PRO	A	425	-4.545	23.118	45.774	1.00	16.63
ATOM	1634	CD	PRO	A	425	-3.694	23.394	44.593	1.00	14.62
ATOM	1635	CA	PRO	A	425	-4.096	21.935	46.484	1.00	18.01
ATOM	1636	CB	PRO	A	425	-2.965	21.392	45.635	1.00	17.36
ATOM	1637	CG	PRO	A	425	-3.064	22.047	44.301	1.00	16.07
ATOM	1638	C	PRO	A	425	-3.655	22.217	47.908	1.00	19.52
ATOM	1639	O	PRO	A	425	-3.304	23.325	48.294	1.00	16.80
ATOM	1640	N	ASN	A	426	-3.670	21.143	48.707	1.00	21.90
ATOM	1641	ND2	ASN	A	426	-6.177	19.346	50.674	1.00	32.22
ATOM	1642	OD1	ASN	A	426	-5.934	21.437	51.378	1.00	30.53
ATOM	1643	CG	ASN	A	426	-5.407	20.380	51.018	1.00	30.42
ATOM	1644	CB	ASN	A	426	-3.898	20.167	50.928	1.00	27.25
ATOM	1645	CA	ASN	A	426	-3.224	21.249	50.088	1.00	24.17
ATOM	1646	C	ASN	A	426	-1.695	21.270	50.121	1.00	22.87
ATOM	1647	O	ASN	A	426	-1.014	21.025	49.127	1.00	19.72
ATOM	1648	N	GLU	A	427	-1.148	21.695	51.247	1.00	24.03
ATOM	1649	OE2	GLU	A	427	3.209	21.859	55.259	1.00	39.86
ATOM	1650	OE1	GLU	A	427	2.503	23.818	54.605	1.00	37.70
ATOM	1651	CD	GLU	A	427	2.640	22.595	54.427	1.00	37.41
ATOM	1652	CG	GLU	A	427	2.167	21.979	53.132	1.00	36.42
ATOM	1653	CB	GLU	A	427	0.679	22.110	52.857	1.00	32.16
ATOM	1654	CA	GLU	A	427	0.305	21.775	51.409	1.00	29.42
ATOM	1655	C	GLU	A	427	0.998	20.507	50.975	1.00	29.51
ATOM	1656	O	GLU	A	427	1.971	20.497	50.213	1.00	29.26
ATOM	1657	N	ASP	A	428	0.488	19.358	51.414	1.00	31.72
ATOM	1658	OD2	ASP	A	428	-1.918	16.341	52.011	1.00	41.88
ATOM	1659	OD1	ASP	A	428	-1.452	18.328	52.816	1.00	37.31
ATOM	1660	CG	ASP	A	428	-1.103	17.267	52.267	1.00	38.88
ATOM	1661	CB	ASP	A	428	0.320	16.958	51.853	1.00	36.50

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1662	CA	ASP	A	428	1.042	18.054	51.077	1.00	32.85
ATOM	1663	C	ASP	A	428	1.081	17.735	49.610	1.00	32.15
ATOM	1664	O	ASP	A	428	1.827	16.851	49.173	1.00	32.63
ATOM	1665	N	GLN	A	429	0.302	18.414	48.772	1.00	29.90
ATOM	1666	NE2	GLN	A	429	-0.844	15.151	46.445	1.00	35.05
ATOM	1667	OE1	GLN	A	429	-0.895	15.061	48.694	1.00	36.32
ATOM	1668	CD	GLN	A	429	-1.190	15.629	47.636	1.00	35.53
ATOM	1669	CG	GLN	A	429	-1.923	16.955	47.621	1.00	32.82
ATOM	1670	CB	GLN	A	429	-1.138	18.032	46.865	1.00	30.20
ATOM	1671	CA	GLN	A	429	0.307	18.190	47.347	1.00	26.44
ATOM	1672	C	GLN	A	429	1.041	19.302	46.621	1.00	22.82
ATOM	1673	O	GLN	A	429	0.832	19.463	45.426	1.00	21.67
ATOM	1674	N	GLY	A	430	1.812	20.142	47.320	1.00	18.52
ATOM	1675	CA	GLY	A	430	2.534	21.185	46.583	1.00	15.09
ATOM	1676	C	GLY	A	430	1.982	22.581	46.889	1.00	14.53
ATOM	1677	O	GLY	A	430	2.582	23.559	46.432	1.00	16.43
ATOM	1678	N	GLY	A	431	0.898	22.745	47.615	1.00	11.39
ATOM	1679	CA	GLY	A	431	0.314	24.011	47.958	1.00	12.94
ATOM	1680	C	GLY	A	431	-0.505	24.702	46.871	1.00	10.35
ATOM	1681	O	GLY	A	431	-0.764	24.181	45.795	1.00	11.85
ATOM	1682	N	LYS	A	432	-0.845	25.936	47.147	1.00	11.65
ATOM	1683	CA	LYS	A	432	-1.637	26.762	46.245	1.00	13.87
ATOM	1684	CB	LYS	A	432	-2.343	27.862	47.049	1.00	16.54
ATOM	1685	CG	LYS	A	432	-3.250	27.146	48.043	1.00	20.67
ATOM	1686	CD	LYS	A	432	-4.058	28.036	48.933	1.00	24.37
ATOM	1687	CE	LYS	A	432	-5.090	27.228	49.718	1.00	25.86
ATOM	1688	NZ	LYS	A	432	-4.539	25.962	50.296	1.00	25.58
ATOM	1689	C	LYS	A	432	-0.810	27.312	45.112	1.00	12.71
ATOM	1690	O	LYS	A	432	0.414	27.398	45.187	1.00	11.37
ATOM	1691	N	TYR	A	433	-1.533	27.713	44.072	1.00	8.62
ATOM	1692	CA	TYR	A	433	-0.997	28.243	42.844	1.00	8.63
ATOM	1693	CB	TYR	A	433	-1.677	27.746	41.591	1.00	8.94
ATOM	1694	CG	TYR	A	433	-1.507	26.270	41.276	1.00	12.81
ATOM	1695	CD1	TYR	A	433	-2.460	25.350	41.653	1.00	12.02
ATOM	1696	CE1	TYR	A	433	-2.310	23.999	41.361	1.00	14.63
ATOM	1697	CD2	TYR	A	433	-0.360	25.813	40.637	1.00	13.00
ATOM	1698	CE2	TYR	A	433	-0.202	24.469	40.333	1.00	14.04
ATOM	1699	CZ	TYR	A	433	-1.180	23.579	40.713	1.00	15.76
ATOM	1700	OH	TYR	A	433	-1.018	22.241	40.429	1.00	18.68
ATOM	1701	C	TYR	A	433	-0.990	29.769	42.955	1.00	6.12
ATOM	1702	O	TYR	A	433	-1.576	30.319	43.866	1.00	7.36
ATOM	1703	N	VAL	A	434	-0.279	30.385	42.031	1.00	8.06
ATOM	1704	CA	VAL	A	434	-0.023	31.820	42.080	1.00	9.13
ATOM	1705	CB	VAL	A	434	1.026	32.189	41.035	1.00	9.24
ATOM	1706	CG1	VAL	A	434	0.473	32.255	39.614	1.00	9.78
ATOM	1707	CG2	VAL	A	434	1.656	33.531	41.432	1.00	9.67
ATOM	1708	C	VAL	A	434	-1.247	32.724	41.971	1.00	9.44
ATOM	1709	O	VAL	A	434	-1.224	33.807	42.521	1.00	8.77
ATOM	1710	N	MET	A	435	-2.348	32.242	41.373	1.00	9.61
ATOM	1711	CA	MET	A	435	-3.580	33.044	41.377	1.00	10.35
ATOM	1712	CB	MET	A	435	-4.313	32.866	40.054	1.00	9.92
ATOM	1713	CG	MET	A	435	-3.514	33.300	38.848	1.00	10.91
ATOM	1714	SD	MET	A	435	-2.789	34.945	38.866	1.00	11.06
ATOM	1715	CE	MET	A	435	-4.229	35.954	39.266	1.00	11.66

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1716	C	MET	A	435	-4.479	32.835	42.569	1.00	11.89
ATOM	1717	O	MET	A	435	-5.625	33.382	42.578	1.00	10.19
ATOM	1718	N	TYR	A	436	-4.004	32.200	43.636	1.00	9.70
ATOM	1719	CA	TYR	A	436	-4.776	32.133	44.873	1.00	10.59
ATOM	1720	CB	TYR	A	436	-4.154	31.274	45.976	1.00	12.19
ATOM	1721	CG	TYR	A	436	-5.187	30.700	46.929	1.00	12.41
ATOM	1722	CD1	TYR	A	436	-6.086	29.710	46.528	1.00	13.54
ATOM	1723	CE1	TYR	A	436	-7.026	29.190	47.405	1.00	10.84
ATOM	1724	CD2	TYR	A	436	-5.275	31.200	48.218	1.00	12.72
ATOM	1725	CE2	TYR	A	436	-6.216	30.710	49.104	1.00	15.95
ATOM	1726	CZ	TYR	A	436	-7.105	29.725	48.659	1.00	14.43
ATOM	1727	OH	TYR	A	436	-8.012	29.268	49.572	1.00	17.14
ATOM	1728	C	TYR	A	436	-4.977	33.571	45.304	1.00	10.80
ATOM	1729	O	TYR	A	436	-4.106	34.412	45.121	1.00	7.79
ATOM	1730	N	PRO	A	437	-6.178	33.938	45.778	1.00	11.93
ATOM	1731	CD	PRO	A	437	-7.340	33.037	45.939	1.00	11.26
ATOM	1732	CA	PRO	A	437	-6.467	35.326	46.139	1.00	10.62
ATOM	1733	CB	PRO	A	437	-7.962	35.319	46.495	1.00	12.25
ATOM	1734	CG	PRO	A	437	-8.320	33.884	46.714	1.00	12.44
ATOM	1735	C	PRO	A	437	-5.713	35.775	47.385	1.00	10.79
ATOM	1736	O	PRO	A	437	-5.577	36.995	47.602	1.00	11.50
ATOM	1737	N	ILE	A	438	-5.411	34.802	48.243	1.00	11.06
ATOM	1738	CA	ILE	A	438	-4.645	35.046	49.464	1.00	14.21
ATOM	1739	CB	ILE	A	438	-5.154	34.201	50.625	1.00	16.10
ATOM	1740	CG2	ILE	A	438	-4.290	34.449	51.876	1.00	19.74
ATOM	1741	CG1	ILE	A	438	-6.619	34.470	50.967	1.00	19.29
ATOM	1742	CD1	ILE	A	438	-7.175	33.545	52.055	1.00	20.13
ATOM	1743	C	ILE	A	438	-3.173	34.778	49.119	1.00	14.66
ATOM	1744	O	ILE	A	438	-2.796	33.666	48.710	1.00	10.76
ATOM	1745	N	ALA	A	439	-2.342	35.803	49.202	1.00	12.90
ATOM	1746	CB	ALA	A	439	-0.137	36.968	49.129	1.00	13.51
ATOM	1747	CA	ALA	A	439	-0.946	35.702	48.748	1.00	12.56
ATOM	1748	C	ALA	A	439	-0.219	34.450	49.179	1.00	11.82
ATOM	1749	O	ALA	A	439	-0.053	34.221	50.350	1.00	12.72
ATOM	1750	N	VAL	A	440	0.244	33.624	48.232	1.00	12.54
ATOM	1751	CA	VAL	A	440	1.038	32.460	48.610	1.00	13.18
ATOM	1752	CB	VAL	A	440	1.194	31.545	47.405	1.00	13.89
ATOM	1753	CG1	VAL	A	440	-0.203	30.964	47.060	1.00	14.71
ATOM	1754	CG2	VAL	A	440	1.748	32.335	46.225	1.00	14.29
ATOM	1755	C	VAL	A	440	2.422	32.915	49.105	1.00	13.24
ATOM	1756	O	VAL	A	440	2.951	33.937	48.665	1.00	10.97
ATOM	1757	N	SER	A	441	3.009	32.117	49.958	1.00	13.77
ATOM	1758	CA	SER	A	441	4.320	32.448	50.541	1.00	15.67
ATOM	1759	CB	SER	A	441	4.602	31.531	51.741	1.00	14.54
ATOM	1760	OG	SER	A	441	4.895	30.230	51.251	1.00	12.13
ATOM	1761	C	SER	A	441	5.443	32.298	49.543	1.00	14.86
ATOM	1762	O	SER	A	441	6.393	33.042	49.627	1.00	16.15
ATOM	1763	N	GLY	A	442	5.365	31.340	48.626	1.00	15.69
ATOM	1764	CA	GLY	A	442	6.458	31.086	47.680	1.00	15.78
ATOM	1765	C	GLY	A	442	7.329	29.955	48.292	1.00	17.87
ATOM	1766	O	GLY	A	442	8.313	29.533	47.700	1.00	17.88
ATOM	1767	N	ASP	A	443	6.933	29.420	49.433	1.00	16.97
ATOM	1768	CA	ASP	A	443	7.639	28.297	50.053	1.00	19.48
ATOM	1769	CB	ASP	A	443	7.315	28.159	51.522	1.00	20.17

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1770	CG	ASP	A	443	7.612	29.371	52.357	1.00	23.62
ATOM	1771	OD1	ASP	A	443	8.296	30.306	51.896	1.00	23.81
ATOM	1772	OD2	ASP	A	443	7.119	29.399	53.505	1.00	25.54
ATOM	1773	C	ASP	A	443	7.308	26.945	49.435	1.00	21.78
ATOM	1774	O	ASP	A	443	8.052	25.962	49.619	1.00	20.22
ATOM	1775	N	HIS	A	444	6.163	26.878	48.737	1.00	18.42
ATOM	1776	CA	HIS	A	444	5.734	25.593	48.195	1.00	18.25
ATOM	1777	CB	HIS	A	444	4.263	25.329	48.628	1.00	19.33
ATOM	1778	CG	HIS	A	444	4.010	25.631	50.066	1.00	21.40
ATOM	1779	CD2	HIS	A	444	3.475	26.703	50.697	1.00	21.56
ATOM	1780	ND1	HIS	A	444	4.407	24.766	51.066	1.00	22.82
ATOM	1781	CE1	HIS	A	444	4.098	25.274	52.242	1.00	22.65
ATOM	1782	NE2	HIS	A	444	3.540	26.457	52.047	1.00	23.53
ATOM	1783	C	HIS	A	444	5.869	25.478	46.699	1.00	18.20
ATOM	1784	O	HIS	A	444	5.869	26.430	45.924	1.00	16.89
ATOM	1785	N	GLU	A	445	5.967	24.246	46.228	1.00	18.90
ATOM	1786	OE2	GLU	A	445	7.287	19.466	44.909	1.00	37.32
ATOM	1787	OE1	GLU	A	445	5.382	19.436	43.805	1.00	36.75
ATOM	1788	CD	GLU	A	445	6.406	20.025	44.213	1.00	34.73
ATOM	1789	CG	GLU	A	445	6.551	21.509	43.912	1.00	31.48
ATOM	1790	CB	GLU	A	445	5.641	22.370	44.753	1.00	24.36
ATOM	1791	CA	GLU	A	445	6.094	23.856	44.844	1.00	21.30
ATOM	1792	C	GLU	A	445	5.192	24.573	43.856	1.00	19.12
ATOM	1793	O	GLU	A	445	5.654	25.106	42.852	1.00	18.43
ATOM	1794	N	ASN	A	446	3.886	24.568	44.155	1.00	14.02
ATOM	1795	CA	ASN	A	446	2.931	25.161	43.217	1.00	12.89
ATOM	1796	CB	ASN	A	446	1.558	24.575	43.616	1.00	13.52
ATOM	1797	CG	ASN	A	446	1.492	23.081	43.416	1.00	11.57
ATOM	1798	OD1	ASN	A	446	2.288	22.530	42.688	1.00	14.69
ATOM	1799	ND2	ASN	A	446	0.580	22.359	44.016	1.00	14.47
ATOM	1800	C	ASN	A	446	2.880	26.669	43.236	1.00	12.30
ATOM	1801	O	ASN	A	446	2.299	27.295	42.349	1.00	11.18
ATOM	1802	N	ASN	A	447	3.432	27.299	44.274	1.00	12.22
ATOM	1803	CA	ASN	A	447	3.261	28.692	44.560	1.00	12.81
ATOM	1804	CB	ASN	A	447	3.943	29.244	45.794	1.00	13.02
ATOM	1805	CG	ASN	A	447	3.432	28.721	47.094	1.00	14.61
ATOM	1806	OD1	ASN	A	447	4.151	28.922	48.081	1.00	15.02
ATOM	1807	ND2	ASN	A	447	2.276	28.070	47.103	1.00	13.05
ATOM	1808	C	ASN	A	447	3.662	29.596	43.403	1.00	14.50
ATOM	1809	O	ASN	A	447	2.990	30.597	43.173	1.00	14.90
ATOM	1810	N	LYS	A	448	4.698	29.182	42.678	1.00	15.41
ATOM	1811	CA	LYS	A	448	5.123	30.032	41.582	1.00	19.44
ATOM	1812	CB	LYS	A	448	6.678	30.007	41.496	1.00	20.29
ATOM	1813	CG	LYS	A	448	7.319	30.599	42.725	1.00	22.70
ATOM	1814	CD	LYS	A	448	8.503	31.527	42.408	1.00	25.96
ATOM	1815	CE	LYS	A	448	8.285	32.968	42.835	1.00	24.34
ATOM	1816	NZ	LYS	A	448	8.963	33.438	44.090	1.00	16.70
ATOM	1817	C	LYS	A	448	4.568	29.566	40.271	1.00	19.62
ATOM	1818	O	LYS	A	448	5.136	29.990	39.263	1.00	25.92
ATOM	1819	N	MET	A	449	3.632	28.647	40.230	1.00	13.54
ATOM	1820	CA	MET	A	449	3.122	28.149	38.956	1.00	14.78
ATOM	1821	CB	MET	A	449	3.181	26.610	39.000	1.00	17.23
ATOM	1822	CG	MET	A	449	4.638	26.182	39.231	1.00	23.71
ATOM	1823	SD	MET	A	449	5.557	26.266	37.701	1.00	35.18

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1824	CE	MET	A	449	6.512	27.753	37.876	1.00	29.45
ATOM	1825	C	MET	A	449	1.660	28.558	38.779	1.00	10.74
ATOM	1826	O	MET	A	449	1.051	28.898	39.776	1.00	7.03
ATOM	1827	N	PHE	A	450	1.104	28.330	37.629	1.00	9.72
ATOM	1828	CA	PHE	A	450	-0.319	28.583	37.393	1.00	11.38
ATOM	1829	CB	PHE	A	450	-0.503	29.170	35.975	1.00	11.13
ATOM	1830	CG	PHE	A	450	-0.071	30.631	35.959	1.00	12.52
ATOM	1831	CD1	PHE	A	450	-0.930	31.655	36.320	1.00	12.19
ATOM	1832	CD2	PHE	A	450	1.207	30.955	35.549	1.00	10.84
ATOM	1833	CE1	PHE	A	450	-0.508	32.973	36.265	1.00	11.08
ATOM	1834	CE2	PHE	A	450	1.624	32.264	35.490	1.00	10.58
ATOM	1835	CZ	PHE	A	450	0.770	33.283	35.856	1.00	10.00
ATOM	1836	C	PHE	A	450	-1.150	27.312	37.490	1.00	11.07
ATOM	1837	O	PHE	A	450	-0.799	26.260	36.954	1.00	9.07
ATOM	1838	N	SER	A	451	-2.323	27.410	38.138	1.00	11.36
ATOM	1839	CA	SER	A	451	-3.268	26.315	38.270	1.00	10.14
ATOM	1840	CB	SER	A	451	-4.487	26.735	39.155	1.00	10.95
ATOM	1841	OG	SER	A	451	-5.179	27.782	38.420	1.00	9.02
ATOM	1842	C	SER	A	451	-3.844	25.958	36.901	1.00	9.35
ATOM	1843	O	SER	A	451	-3.770	26.735	35.963	1.00	9.40
ATOM	1844	N	GLN	A	452	-4.577	24.855	36.824	1.00	12.16
ATOM	1845	CA	GLN	A	452	-5.351	24.521	35.618	1.00	13.47
ATOM	1846	CB	GLN	A	452	-5.964	23.125	35.803	1.00	16.94
ATOM	1847	CG	GLN	A	452	-6.700	22.595	34.601	1.00	21.50
ATOM	1848	CD	GLN	A	452	-5.827	22.669	33.361	1.00	23.04
ATOM	1849	OE1	GLN	A	452	-4.673	22.244	33.400	1.00	21.47
ATOM	1850	NE2	GLN	A	452	-6.377	23.285	32.307	1.00	23.25
ATOM	1851	C	GLN	A	452	-6.430	25.554	35.338	1.00	13.65
ATOM	1852	O	GLN	A	452	-6.638	25.907	34.165	1.00	14.17
ATOM	1853	N	CYS	A	453	-7.045	26.104	36.363	1.00	14.02
ATOM	1854	CA	CYS	A	453	-8.092	27.127	36.197	1.00	17.31
ATOM	1855	CB	CYS	A	453	-8.719	27.417	37.560	1.00	21.49
ATOM	1856	SG	CYS	A	453	-9.533	26.093	38.447	1.00	29.58
ATOM	1857	C	CYS	A	453	-7.500	28.361	35.535	1.00	15.91
ATOM	1858	O	CYS	A	453	-7.993	28.886	34.524	1.00	12.98
ATOM	1859	N	SER	A	454	-6.301	28.786	36.002	1.00	10.78
ATOM	1860	CA	SER	A	454	-5.584	29.858	35.390	1.00	9.42
ATOM	1861	CB	SER	A	454	-4.341	30.410	36.146	1.00	8.01
ATOM	1862	OG	SER	A	454	-4.692	30.709	37.471	1.00	8.77
ATOM	1863	C	SER	A	454	-5.186	29.538	33.979	1.00	9.67
ATOM	1864	O	SER	A	454	-5.237	30.413	33.113	1.00	9.80
ATOM	1865	N	LYS	A	455	-4.691	28.304	33.763	1.00	11.07
ATOM	1866	CA	LYS	A	455	-4.240	27.987	32.421	1.00	12.98
ATOM	1867	CB	LYS	A	455	-3.599	26.587	32.376	1.00	13.14
ATOM	1868	CG	LYS	A	455	-2.146	26.611	32.855	1.00	17.01
ATOM	1869	CD	LYS	A	455	-1.656	25.166	32.882	1.00	19.15
ATOM	1870	CE	LYS	A	455	-0.242	25.104	33.451	1.00	20.39
ATOM	1871	NZ	LYS	A	455	0.195	23.673	33.295	1.00	23.90
ATOM	1872	C	LYS	A	455	-5.367	28.049	31.401	1.00	12.31
ATOM	1873	O	LYS	A	455	-5.180	28.539	30.315	1.00	12.74
ATOM	1874	N	GLN	A	456	-6.529	27.527	31.755	1.00	14.47
ATOM	1875	NE2	GLN	A	456	-10.676	25.407	33.099	1.00	30.34
ATOM	1876	OE1	GLN	A	456	-9.503	23.500	32.899	1.00	29.79
ATOM	1877	CD	GLN	A	456	-9.664	24.686	32.606	1.00	28.31

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1878	CG	GLN	A	456	-8.670	25.342	31.686	1.00	25.00
ATOM	1879	CB	GLN	A	456	-8.814	26.832	31.511	1.00	19.95
ATOM	1880	CA	GLN	A	456	-7.661	27.516	30.804	1.00	16.41
ATOM	1881	C	GLN	A	456	-7.967	28.942	30.401	1.00	15.24
ATOM	1882	O	GLN	A	456	-7.936	29.330	29.244	1.00	15.99
ATOM	1883	N	SER	A	457	-8.038	29.821	31.393	1.00	14.14
ATOM	1884	CA	SER	A	457	-8.377	31.231	31.194	1.00	14.81
ATOM	1885	CB	SER	A	457	-8.518	31.976	32.530	1.00	15.12
ATOM	1886	OG	SER	A	457	-9.565	31.464	33.315	1.00	16.45
ATOM	1887	C	SER	A	457	-7.354	31.967	30.377	1.00	12.94
ATOM	1888	O	SER	A	457	-7.697	32.696	29.467	1.00	12.19
ATOM	1889	N	ILE	A	458	-6.051	31.825	30.722	1.00	12.21
ATOM	1890	CA	ILE	A	458	-5.038	32.567	29.982	1.00	9.86
ATOM	1891	CB	ILE	A	458	-3.699	32.500	30.795	1.00	11.36
ATOM	1892	CG2	ILE	A	458	-2.555	32.898	29.890	1.00	6.36
ATOM	1893	CG1	ILE	A	458	-3.853	33.384	32.036	1.00	9.88
ATOM	1894	CD1	ILE	A	458	-2.730	33.281	33.059	1.00	11.89
ATOM	1895	C	ILE	A	458	-4.854	32.048	28.573	1.00	9.53
ATOM	1896	O	ILE	A	458	-4.640	32.816	27.634	1.00	9.61
ATOM	1897	N	TYR	A	459	-4.939	30.731	28.423	1.00	9.48
ATOM	1898	CA	TYR	A	459	-4.767	30.100	27.112	1.00	11.60
ATOM	1899	CB	TYR	A	459	-5.038	28.600	27.250	1.00	11.22
ATOM	1900	CG	TYR	A	459	-5.045	27.843	25.943	1.00	16.31
ATOM	1901	CD1	TYR	A	459	-4.013	27.976	25.041	1.00	16.99
ATOM	1902	CE1	TYR	A	459	-4.028	27.303	23.827	1.00	19.40
ATOM	1903	CD2	TYR	A	459	-6.103	26.999	25.626	1.00	18.93
ATOM	1904	CE2	TYR	A	459	-6.108	26.299	24.422	1.00	21.51
ATOM	1905	CZ	TYR	A	459	-5.075	26.458	23.532	1.00	20.71
ATOM	1906	OH	TYR	A	459	-5.095	25.772	22.341	1.00	21.74
ATOM	1907	C	TYR	A	459	-5.720	30.750	26.110	1.00	12.72
ATOM	1908	O	TYR	A	459	-5.334	31.252	25.073	1.00	14.82
ATOM	1909	N	LYS	A	460	-6.974	30.779	26.528	1.00	14.14
ATOM	1910	NZ	LYS	A	460	-10.468	26.961	25.743	1.00	30.41
ATOM	1911	CE	LYS	A	460	-9.733	27.718	24.702	1.00	27.82
ATOM	1912	CD	LYS	A	460	-9.809	29.219	24.921	1.00	26.35
ATOM	1913	CG	LYS	A	460	-9.794	29.689	26.345	1.00	23.26
ATOM	1914	CB	LYS	A	460	-9.375	31.156	26.477	1.00	19.80
ATOM	1915	CA	LYS	A	460	-8.043	31.371	25.721	1.00	18.07
ATOM	1916	C	LYS	A	460	-7.739	32.806	25.384	1.00	16.65
ATOM	1917	O	LYS	A	460	-7.735	33.206	24.228	1.00	16.84
ATOM	1918	N	THR	A	461	-7.225	33.546	26.348	1.00	14.44
ATOM	1919	CA	THR	A	461	-6.847	34.932	26.129	1.00	14.79
ATOM	1920	CB	THR	A	461	-6.597	35.590	27.509	1.00	13.79
ATOM	1921	OG1	THR	A	461	-7.813	35.528	28.254	1.00	13.87
ATOM	1922	CG2	THR	A	461	-6.192	37.054	27.345	1.00	16.01
ATOM	1923	C	THR	A	461	-5.709	35.061	25.159	1.00	14.88
ATOM	1924	O	THR	A	461	-5.830	35.765	24.142	1.00	14.86
ATOM	1925	N	ILE	A	462	-4.569	34.417	25.419	1.00	14.52
ATOM	1926	CA	ILE	A	462	-3.422	34.528	24.542	1.00	17.34
ATOM	1927	CB	ILE	A	462	-2.223	33.642	24.975	1.00	18.43
ATOM	1928	CG2	ILE	A	462	-1.130	33.699	23.904	1.00	20.28
ATOM	1929	CG1	ILE	A	462	-1.643	34.018	26.316	1.00	18.70
ATOM	1930	CD1	ILE	A	462	-0.726	32.967	26.946	1.00	19.10
ATOM	1931	C	ILE	A	462	-3.757	34.102	23.124	1.00	18.59

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1932	O	ILE	A	462	-3.420	34.813	22.189	1.00	17.11
ATOM	1933	N	GLU	A	463	-4.473	32.979	22.968	1.00	22.82
ATOM	1934	OE2	GLU	A	463	-8.026	29.422	22.532	1.00	41.03
ATOM	1935	OE1	GLU	A	463	-7.006	28.787	20.674	1.00	39.73
ATOM	1936	CD	GLU	A	463	-7.293	29.635	21.536	1.00	39.22
ATOM	1937	CG	GLU	A	463	-6.723	31.032	21.405	1.00	36.15
ATOM	1938	CB	GLU	A	463	-5.228	31.095	21.624	1.00	30.56
ATOM	1939	CA	GLU	A	463	-4.692	32.520	21.587	1.00	26.30
ATOM	1940	C	GLU	A	463	-5.492	33.530	20.800	1.00	27.72
ATOM	1941	O	GLU	A	463	-5.233	33.704	19.607	1.00	29.03
ATOM	1942	N	SER	A	464	-6.399	34.283	21.418	1.00	26.79
ATOM	1943	CA	SER	A	464	-7.190	35.312	20.764	1.00	26.80
ATOM	1944	CB	SER	A	464	-8.395	35.611	21.666	1.00	25.15
ATOM	1945	OG	SER	A	464	-9.060	36.806	21.404	1.00	25.60
ATOM	1946	C	SER	A	464	-6.434	36.623	20.582	1.00	27.79
ATOM	1947	O	SER	A	464	-6.686	37.340	19.612	1.00	27.52
ATOM	1948	N	LYS	A	465	-5.598	36.959	21.560	1.00	25.83
ATOM	1949	CA	LYS	A	465	-4.956	38.267	21.585	1.00	28.04
ATOM	1950	CB	LYS	A	465	-5.065	38.846	22.993	1.00	28.65
ATOM	1951	CG	LYS	A	465	-6.217	39.766	23.316	1.00	30.43
ATOM	1952	CD	LYS	A	465	-7.570	39.136	23.099	1.00	31.72
ATOM	1953	CE	LYS	A	465	-8.699	40.165	23.068	1.00	32.17
ATOM	1954	NZ	LYS	A	465	-8.593	41.165	24.149	1.00	32.20
ATOM	1955	C	LYS	A	465	-3.505	38.293	21.145	1.00	27.28
ATOM	1956	O	LYS	A	465	-3.053	39.353	20.704	1.00	27.45
ATOM	1957	N	ALA	A	466	-2.767	37.193	21.184	1.00	28.49
ATOM	1958	CA	ALA	A	466	-1.373	37.191	20.753	1.00	28.95
ATOM	1959	CB	ALA	A	466	-0.788	35.788	20.750	1.00	27.44
ATOM	1960	C	ALA	A	466	-1.152	37.821	19.385	1.00	30.12
ATOM	1961	O	ALA	A	466	-0.295	38.708	19.256	1.00	28.37
ATOM	1962	N	GLN	A	467	-1.922	37.440	18.373	1.00	30.63
ATOM	1963	NE2	GLN	A	467	0.360	36.582	14.061	1.00	41.77
ATOM	1964	OE1	GLN	A	467	-0.196	35.394	15.846	1.00	42.22
ATOM	1965	CD	GLN	A	467	-0.524	36.191	14.967	1.00	40.84
ATOM	1966	CG	GLN	A	467	-1.903	36.768	14.813	1.00	40.14
ATOM	1967	CB	GLN	A	467	-2.609	37.306	16.027	1.00	36.55
ATOM	1968	CA	GLN	A	467	-1.712	38.007	17.038	1.00	33.94
ATOM	1969	C	GLN	A	467	-1.891	39.519	16.996	1.00	33.19
ATOM	1970	O	GLN	A	467	-1.208	40.231	16.271	1.00	33.32
ATOM	1971	N	GLU	A	468	-2.797	40.063	17.768	1.00	33.44
ATOM	1972	OE2	GLU	A	468	-7.657	40.802	18.969	1.00	44.61
ATOM	1973	OE1	GLU	A	468	-6.465	41.900	20.497	1.00	44.24
ATOM	1974	CD	GLU	A	468	-6.664	41.480	19.332	1.00	44.10
ATOM	1975	CG	GLU	A	468	-5.602	41.832	18.305	1.00	41.64
ATOM	1976	CB	GLU	A	468	-4.238	41.582	18.934	1.00	38.28
ATOM	1977	CA	GLU	A	468	-3.092	41.457	17.917	1.00	35.15
ATOM	1978	C	GLU	A	468	-1.956	42.299	18.485	1.00	33.88
ATOM	1979	O	GLU	A	468	-1.706	43.397	17.980	1.00	32.88
ATOM	1980	N	CYS	A	469	-1.382	41.873	19.618	1.00	32.54
ATOM	1981	CA	CYS	A	469	-0.374	42.738	20.230	1.00	32.43
ATOM	1982	CB	CYS	A	469	-1.019	43.591	21.320	1.00	34.38
ATOM	1983	SG	CYS	A	469	-1.294	42.874	22.918	1.00	36.46
ATOM	1984	C	CYS	A	469	0.888	42.055	20.713	1.00	29.85
ATOM	1985	O	CYS	A	469	1.786	42.811	21.105	1.00	30.62

		Atom Type	Residue	?	#	X	Y	Z	OCC	B
ATOM	1986	N	PHE	A	470	1.027	40.739	20.624	1.00	26.22
ATOM	1987	CA	PHE	A	470	2.314	40.147	21.073	1.00	25.07
ATOM	1988	CB	PHE	A	470	2.163	38.694	21.471	1.00	21.88
ATOM	1989	CG	PHE	A	470	1.492	38.480	22.808	1.00	21.60
ATOM	1990	CD1	PHE	A	470	0.810	39.497	23.450	1.00	19.78
ATOM	1991	CD2	PHE	A	470	1.556	37.251	23.414	1.00	19.41
ATOM	1992	CE1	PHE	A	470	0.182	39.309	24.658	1.00	20.26
ATOM	1993	CE2	PHE	A	470	0.932	37.046	24.634	1.00	20.13
ATOM	1994	CZ	PHE	A	470	0.257	38.065	25.257	1.00	20.62
ATOM	1995	C	PHE	A	470	3.351	40.383	19.999	1.00	24.85
ATOM	1996	O	PHE	A	470	2.994	40.592	18.836	1.00	23.37
ATOM	1997	N	GLN	A	471	4.610	40.404	20.389	1.00	23.76
ATOM	1998	CA	GLN	A	471	5.714	40.672	19.491	1.00	25.96
ATOM	1999	CB	GLN	A	471	6.350	42.028	19.794	1.00	27.26
ATOM	2000	CG	GLN	A	471	5.453	43.201	19.442	1.00	31.81
ATOM	2001	CD	GLN	A	471	6.014	44.575	19.678	1.00	33.37
ATOM	2002	OE1	GLN	A	471	5.258	45.547	19.668	1.00	35.13
ATOM	2003	NE2	GLN	A	471	7.323	44.723	19.885	1.00	35.41
ATOM	2004	C	GLN	A	471	6.772	39.578	19.615	1.00	25.85
ATOM	2005	O	GLN	A	471	6.668	38.670	20.433	1.00	23.32
ATOM	2006	N	GLU	A	472	7.771	39.683	18.760	1.00	27.21
ATOM	2007	OE2	GLU	A	472	8.898	41.817	17.307	1.00	43.27
ATOM	2008	OE1	GLU	A	472	9.685	41.624	15.282	1.00	44.72
ATOM	2009	CD	GLU	A	472	9.267	41.115	16.344	1.00	42.17
ATOM	2010	CG	GLU	A	472	9.207	39.605	16.387	1.00	39.41
ATOM	2011	CB	GLU	A	472	9.836	38.975	17.600	1.00	34.14
ATOM	2012	CA	GLU	A	472	8.867	38.730	18.759	1.00	30.87
ATOM	2013	C	GLU	A	472	9.656	38.993	20.037	1.00	30.26
ATOM	2014	O	GLU	A	472	9.773	40.161	20.396	1.00	29.23
ATOM	2015	N	ARG	A	473	10.256	37.970	20.584	1.00	31.97
ATOM	2016	CA	ARG	A	473	11.073	38.106	21.778	1.00	34.21
ATOM	2017	CB	ARG	A	473	11.230	36.691	22.340	1.00	34.97
ATOM	2018	CG	ARG	A	473	12.230	36.454	23.443	1.00	37.52
ATOM	2019	CD	ARG	A	473	11.661	35.449	24.436	1.00	39.68
ATOM	2020	NE	ARG	A	473	12.564	35.155	25.532	1.00	41.06
ATOM	2021	CZ	ARG	A	473	12.469	35.726	26.729	1.00	42.18
ATOM	2022	NH1	ARG	A	473	13.327	35.423	27.693	1.00	42.83
ATOM	2023	NH2	ARG	A	473	11.559	36.660	26.960	1.00	42.33
ATOM	2024	C	ARG	A	473	12.451	38.665	21.456	1.00	36.39
ATOM	2025	O	ARG	A	473	13.092	38.294	20.489	1.00	36.44
ATOM	2026	N	SER	A	474	12.918	39.567	22.276	1.00	37.92
ATOM	2027	OG	SER	A	474	15.308	38.413	23.524	1.00	36.38
ATOM	2028	CB	SER	A	474	15.293	39.122	22.290	1.00	37.61
ATOM	2029	CA	SER	A	474	14.200	40.202	22.359	1.00	37.96
ATOM	2030	C	SER	A	474	14.436	41.341	21.403	1.00	39.67
ATOM	2031	O	SER	A	474	13.589	42.259	21.336	1.00	40.16
END										

Example 5 - TACE Inhibitor Design

The TACE x-ray diffraction coordinates were read into a Sybyl v.6.3 (Tripos Associates) software package and the x-ray structure analyzed graphically. The regions within the original x-ray coordinates were corrected for chirality and atom type. The modified x-ray model of TACE was energy minimized until all the TACE structural parameters were at their equilibrium or optimal values. The energy minimized structure was then compared to the original structure to confirm the absence of anomalies.

Sites of specific interaction(s) between TACE and the co-crystallized inhibitor were identified. The inhibitor was then removed from the X-ray complex model, leaving only the TACE structural model.

Candidate inhibitors were chosen based upon the sites of interaction with TACE and the candidate inhibitor in light of the sites of interaction identified previously for the co-crystallized inhibitor. Once specific candidate inhibitor-TACE interactions were determined, docking studies were performed to provide preliminary "modeled" complexes of selected candidate inhibitors with TACE.

Constrained conformational analysis was performed using molecular dynamics (MD) to check the integrity of the modeled TACE-inhibitor complex. Once the complex reached its most favorable conformational state, the structure as proposed by the MD study was analyzed visually to insure that the modeled complex complied with known experimental SAR/QSAR based on measured binding affinities.

The modeled candidate inhibitor-TACE complex was analyzed. The region of the complex associated with the S1' regions of TACE containing a small solvent exposed channel was chosen as a target region for modification. A single modification, a benzyl group which becomes embedded within the target region, was selected based upon computational and synthetic chemical principles. The benzyl group was oriented on an appropriate zinc chelator core so as to be projected

into the S1' S3' pocket. This modification converts an inhibitor which was generally MMP selective to one which is TACE selective. IC50 data for the inhibitor with a benzyl modification confirm this selectivity.

Structure-based analoging for optimization of inhibitor potency, selectivity and physical drug-like properties was performed in an iterative manner.

Example 6 - Measuring TACE Inhibition

250μM peptide substrate (Ac-SPLAQAVRSSSR-NH_2) was incubate with 3.7 U/μL TACE in a buffer containing 10mM TRIS HCl, pH 7.4, 10% glycerol at 25 degrees C. The reaction was quenched with 1% TFA (final concentration) after two hours. The reaction mixture was separated by HPLC on a Hewlett-Packard 1150. The product formation was monitored by absorbance at 220nm.

The linearity of the reaction was confirmed ($r^2 > 0.85$). The mean ($x \pm$ sem) of the control rate was calculated and compared for statistical significance ($p < 0.05$) with drug-tested rates using Dunnett's multiple comparison test. Dose-response relationships were generated using multiple doses of drug and IC_{50} values with 95% CI were estimated using linear regression.

From the foregoing description and examples, one skilled in the art can ascertain the essential characteristics of the invention and, without departing from the spirit and scope of the invention, can make changes, modifications, and variations of the invention to adapt it to various uses and conditions. Additionally, the disclosure of all publications and patent applications cited above, including U.S. provisional patent application serial No. 60/073,709; U.S. patent application serial No. 09/050,083; and US provisional patent application titled "Crystalline TNF-α-Converting Enzyme and Uses Thereof," filed January 27, 1999, are expressly incorporated herein by reference in their entireties to the same extent as if each were incorporated by reference individually.

What We Claim Is:

1. A composition comprising a polypeptide in crystalline form, wherein the polypeptide is a TNF-α-converting enzyme polypeptide.

2. A composition according to claim 1, wherein the TNF-α-converting enzyme polypeptide comprises the TNF-α-converting enzyme catalytic domain.

3. A composition according to claim 1, wherein the TNF-α-converting enzyme polypeptide is the expression product of a polynucleotide encoding the pro and catalytic domains of TNF-α-converting enzyme.

4. A composition according to claim 1, wherein the TNF-α-converting enzyme polypeptide is the expression product of a polynucleotide encoding the amino acid residues 1-477 of TNF-α-converting enzyme.

5. A composition according to claim 4, wherein the polynucleotide is substituted such that amino acid residue Ser266 is changed to Ala and amino acid residue Asn542 is changed to Gln, and wherein a second polynucleotide encoding the sequence Gly-Ser-$(His)_6$ is fused to the C-terminus.

6. A composition according to claim 1, further comprising a binding partner suitable for co-crystallization with the TNF-α-converting enzyme polypeptide.

7. A composition according to claim 6, wherein the binding partner is a hydroxamate-based binding partner.

8. A composition according to claim 6, wherein the binding partner is N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine,2-(amino)ethyl amide.

9. A composition according to claim 1, wherein the crystal has a crystal structure diffracting to 2.0 Å.

10. A composition according to claim 1, wherein the crystal is monoclinic.

11. A composition according to claim 1, wherein the unit cell of the crystal comprises four crystallographically independent TNF-α-converting enzyme catalytic domain (TCD) molecules.

12. A composition according to claim 11, wherein the TCD molecules are in an asymmetric unit.

13. A composition according to claim 1, wherein the crystal is of monoclinic space group $P2_1$ and the cell has the constants a=61.38 A, b=126.27 A, c=81.27 A, and β=107.41°.

14. A composition according to claim 1, wherein the polypeptide is characterized by the structure coordinates according to Table 1, or a substantial part thereof.

15. A method for crystallizing a TNF-α-converting enzyme polypeptide, comprising:

(A) mixing a solution comprising a TACE polypeptide and a binding partner with a crystallization buffer; and

(B) crystallizing the mixture of step (A) by drop vapor diffusion to form a crystalline precipitate.

16. The method according to claim 15, further comprising:

(C) transferring seeds from the crystalline precipitate formed by the drop vapor diffusion and a crystallization promotor into a mixture of a concentrated solution comprising a TACE polypeptide and binding partner substrate, and a crystallization buffer; and

(D) crystallizing the mixture of step (C) by drop vapor diffusion to form a crystal.

17. The method of claim 15, wherein said crystallization buffer is 0.1M Na Citrate pH 5.4, 20%w/v PEG 4000, and 20% v/v Isopropanol.

18.The method of claim 15 or 16, wherein the binding partner is N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine, 2-(amino)ethyl amide.

18. The method of claims 15, wherein crystallization is at a temperature ranging from 4 to 20 degrees Celsius.

19. The method of claim 15, wherein the solution comprising the TACE polypeptide and the inhibitor is at a concentration of about 5 mg/mL to about 12 mg/mL in a buffer.

20. The method of claim 19, wherein the solution comprising a TACE polypeptide and the binding partner is mixed with the crystallization buffer in a 1:1 ratio.

21. A tumor necrosis factor-α (TNF-α)-converting enzyme crystal made by co-crystallizing a TNF-α-converting enzyme polypeptide with a co-crystallization substrate.

22. A computer-readable medium having recorded thereon x-ray crystallographic coordinate data for the catalytic domain of TNF-α converting enzyme, or a portion thereof.

23. A computer-readable medium having recorded thereon the x-ray crystallographic coordinate data set forth in Table 1, or a portion thereof.

24. A computer-readable medium of claim 22, wherein the medium is selected from the group consisting of a floppy disc, a hard disc, computer tape, RAM, ROM, CD, DVD, a magnetic disk, and an optical disk.

25. A computer-readable medium having recorded thereon machine-readable data, wherein the computer-readable medium, when used in conjunction with a machine programmed with instructions for using the data, is capable of generating image signals for depicting a graphical, three-dimensional representation of a TNF-α converting enzyme polypeptide, or portion thereof.

26. A system for studying a TNF-α converting enzyme polypeptide, said system comprising:

(a) a memory capable of storing information representing at least a portion of a TNF-α converting enzyme polypeptide, wherein said memory comprises at least one first-type storage region, including a set of spatial coordinates specifying a location in a three dimensional space, and at least one second-type storage region comprising information representing a characteristic of one of a plurality of amino acids, said second-type storage regions being logically associated with said first-type storage regions in said memory to represent a geometric arrangement of at least one characteristic of said at least a portion of said TNF-α converting enzyme peptide in said three dimensional space;

(b) a processor coupled to said memory to access said first-type storage regions and said second-type storage regions, wherein the processor generates image signals for depicting a visual image representing three dimensional image of said at least one characteristic of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space based on data from said memory; and

(c) a display coupled to said processor to receive said image signals, wherein the display depicts a visual three dimensional image of said at least one characteristic of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space based on said image signals.

27. A system as set forth in claim 26, wherein said image signals include signals for depicting a visual three dimensional image of a ribbon structure of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space.

28. A system as set forth in claim 26, wherein said image signals include signals for depicting a visual image of a solid model representation of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space.

29. A system as set forth in claim 26, wherein said image signals include signals for depicting a visual three dimensional image of electrostatic surface potential of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space.

30. A system as set forth in claim 26, wherein said image signals include signals for depicting a visual three dimensional stereo image of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space.

31. A system as set forth in claim 26, further comprising:

a storage device capable of storing data representing a geometric arrangement of a characteristic of a composition other than said TNF-α converting enzyme polypeptide; and

an operator interface for receiving instructions from a operator; and wherein said processor is coupled to said storage device and to said operator interface and generates additional image signals for depicting said geometric arrangement of said characteristic of said composition relative to said visual three dimensional image of said at least one characteristic of said at least a portion of said TNF-α converting enzyme polypeptide on said display based on instructions from the operator interface.

32. A system as set forth in claim 31, wherein said storage device is part of said memory.

33. A system as set forth in claim 26, comprising a plurality of first-type and second-type storage regions.

34. A video memory capable of storing information for generating a visual display of at least a portion of a TNF-α converting enzyme polypeptide, said video memory comprising:

(a) at least one first-type storage region, each of said first-type storage regions including a set of spatial coordinates specifying a location in a three dimensional space; and

(b) at least one second-type storage region, each of said second-type storage regions containing information for visually depicting a characteristic of one of a plurality of amino acids; wherein said second-type storage regions are logically associated with said first-type storage regions in said video memory to represent a geometric arrangement of at least one characteristic of said at least a portion of said TNF-α converting enzyme polypeptide in said three dimensional space.

35. A video memory as set forth in claim 34, wherein said second-type storage regions are logically associated with said first-type storage regions in said video memory to represent a geometric arrangement of at least one characteristic of a catalytic domain portion of said TNF-α converting enzyme polypeptide in said three dimensional space.

36. A video memory as set forth in claim 34, wherein said first-type storage regions and said second-type storage regions are regions of a semiconductor memory.

37. A video memory as set forth in claim 34, wherein said first-type storage regions and said second-type storage regions are regions of an optical disk.

38. A video memory as set forth in claim 34, wherein said first-type storage regions and said second-type storage regions are regions of a magnetic memory.

39. A video memory as set forth in claim 34, comprising a plurality of first-type and second-type storage regions.

40. A method of identifying a compound that associates with TNF-α-converting enzyme, comprising:

(A) designing an associating compound for said polypeptide that forms a bond with the TNF-α-converting enzyme catalytic domain based on x-ray diffraction coordinates of a TNF-α-converting enzyme polypeptide crystal;

(B) synthesizing said compound; and

(C) determining the associate capability of said compound with said TNF-α-converting enzyme.

41. The method according to claim 40, wherein said associating compound is an inhibitor, mediator, or other compound that regulates TNF-α-converting enzyme activity.

42. The method of claim 41, wherein said associating compound is a competitive inhibitor, un-competitive inhibitor, or non-competitive inhibitor.

43. The method according to claim 40, wherein the coordinates are the coordinates of Table 1, or a substantial part thereof.

44. The method of claim 40, wherein said TNF-α-converting enzyme polypeptide crystal comprises the TNF-α-converting enzyme catalytic domain.

45. The method of claim 40, wherein said TNF-α-converting enzyme polypeptide is the expression product of a polynucleotide encoding the pro and catalytic domains of TNF-α-converting enzyme.

46. The method of claim 40, wherein said TNF-α-converting enzyme polypeptide is the expression product of a polynucleotide encoding the amino acid residues 1-477 of TNF-α-converting enzyme.

47. The method of claim 46, wherein the polynucleotide is substituted such that amino acid residue Ser266 is changed to Ala and amino acid residue Asn542 is changed to Gln, and wherein a second polynucleotide encoding the sequence Gly-Ser-$(His)_6$ is fused to the C-terminus.

48. The method of claim 40, wherein said TNF-α-converting enzyme polypeptide crystal is co-crystallized with a binding partner.

49. The method of claim 48, wherein the binding partner is a hydroxamate-based binding partner.

50. The method of claim 48, wherein the binding partner is N-{D,L-2-(hydroxyaminocarbonyl)methyl-4-methylpentanoyl}-L-3-amino-2-dimethylbutanoyl-L-alanine,2-(amino)ethyl amide.

51. The method of claim 40, wherein said TNF-α-converting enzyme polypeptide crystal has a crystal structure diffracting to 2.0 Å.

52. The method of claim 40, wherein said TNF-α-converting enzyme polypeptide crystal is monoclinic.

53. The method of claim 40, wherein said TNF-α-converting enzyme polypeptide crystal has a unit cell comprising four crystallographically independent TNF-α-converting enzyme catalytic domain (TCD) molecules.

54. The method of claim 53, wherein the TCD molecules are in an asymmetric unit.

55. The method of claim 40, wherein said TNF-α-converting enzyme polypeptide crystal is of monoclinic space group $P2_1$ and the cell has the constants a=61.38 Å, b=126.27 Å, c=81.27 Å, and β=107.41°.

56. The method of claim 40, wherein the associating compound is designed to associate with the S1' region of TNF-α-converting enzyme.

57. The method of claim 40, wherein the associating compound is designed to associate with the S1'S3' pocket of TNF-α-converting enzyme.

58. The method of claim 40, wherein the associating compound is designed to incorporate a moiety that chelates zinc.

59. The method of claim 40, wherein the associating compound is designed to form a hydrogen bond with Leu348 or Gly349 of TNF-α-converting enzyme.

60. The method of claim 40, wherein the associating compound is designed to introduce a non-polar group which occupies the S1' pocket of TNF-α-converting enzyme.

61. The method of claim 40, wherein the associating compound is designed to introduce a group which lies within the channel joining S1' - S3' pockets of TNF-α-converting enzyme and which makes appropriate van der Waal contact with the channel.

62. The method of claim 40, wherein the associating compound is designed to form a hydrogen bond with Leu348 or Gly349 on the backbone amide groups of TNF-α-converting enzyme.

ABSTRACT OF THE INVENTION

A tumor necrosis factor-α converting enzyme (TACE) is produced, purified, and crystallized. The three-dimensional coordinates of the crystal are obtained by X-ray diffraction. The coordinates can be recorded on a computer readable medium, or are part of a video memory, where they can be used as part of a system for studying for studying TACE. The coordinates are also used in designing, screening, and developing compounds that associate with TACE.

FIGURE 1

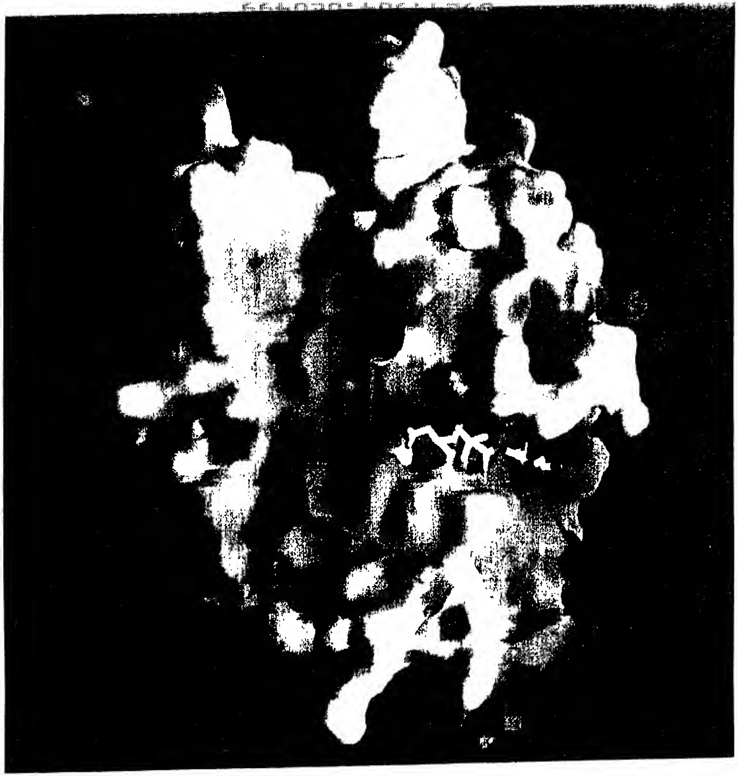


Figure 2A

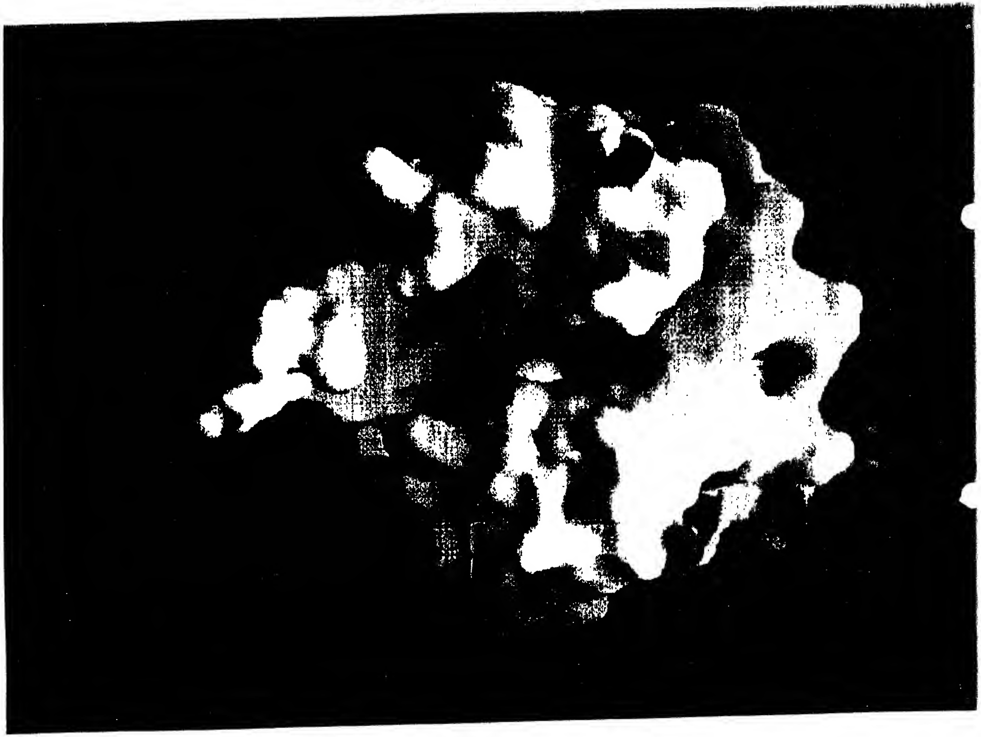


FIGURE
2B

```
ADAM_CROAD        ..........  ......EQNL  PQRYIELVVV  ADRRVFMKYN  .SDLNIIRTR
TACE         205  PEELVHR...  .VKRRADPDP  MKNTCKLLVV  ADHRFYRYMG  RGEESTTTNY  250
hADAM10           QEKHAINGPE  LLRKRRTTSA  EKNTCQLYIQ  TDHLFFKYYG  TRE..AVIAQ

ADAM_CROAD        VHEIVNIINE  FYRSL.....  ...NIRVSLT  DLEIWSGQDF  I......TI.
TACE         251  LIELIDRVDD  IYRNTSWDNA  GFKGYGIQIE  QIRILKSPQE  VKPGEKHYNM  300
hADAM10           ISSHVKAIDT  IYQTT..DFS  GIRNISFMVK  RIRINTTADE  KDPTNPF...

ADAM_CROAD        ..........  QSSSSNTLNS  FGEWRERVLL  TRKRHDNAQL  LTAINFEGKI
TACE         301  AKSYPNEEKD  AWDVKMLLEQ  FSFDIAEEAS  ...KVCLAHL  FTYQDFDMGT  347
hADAM10           ..RFPN....  .ISVEKFLE.  ..LNSEQNHD  ...DYCLAYV  FTDRDFDDGV

ADAM_CROAD        IGKAYTS...  .....SMCNP  ..........  .RSSVGIVKD  HSP....INL
TACE         348  LGLAYVGSPR  ANSHGGVCPK  AYYSPVGKKN  IYLNSGLTST  KNYGKTILTK  397
hADAM10           LGLAWVGAP.  SGSSGGICEK  SKLYSDGKKK  .SLNTGIITV  QNYGSHVPPK

ADAM_CROAD        LVAVTMAHEL  GHNLGMEHDG  K....DCLRG  ........AS  LCIMRPGLTP
TACE         398  EADLVTTHEL  GHNFGAEHDP  DGLAECAPNE  D......QGG  KYVMYPIAVS  441
hADAM10           VSHITFAHEV  GHNFGSPHDS  G..TECTPGE  SKNLGQKENG  NYIMYARATS

ADAM_CROAD        GRS...YEFS  DDSMGYYQKF  LNQYKPQCIL  NKP.......  ..........
TACE         442  GDHENNKMFS  NCSKQSIYKT  IESKAQECFQ  ERSNKVCGNS  RVDEGEECDP  491
hADAM10           GDKLNNNKFS  LCSIRNISQV  LEKKRNNCFV  ESGQPICGNG  MVEQGEECDC
```

FIGURE 3

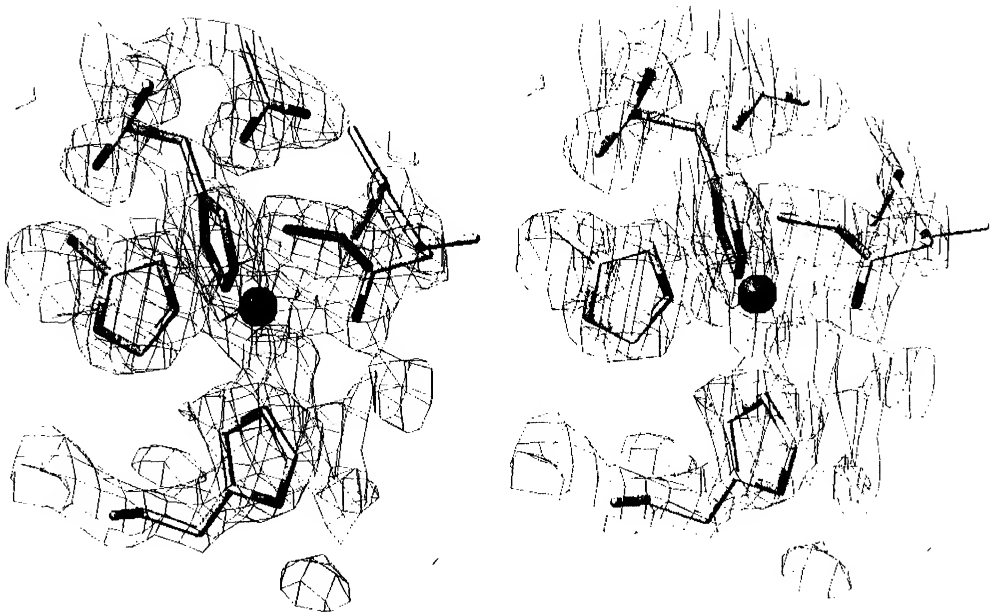


FIGURE 4

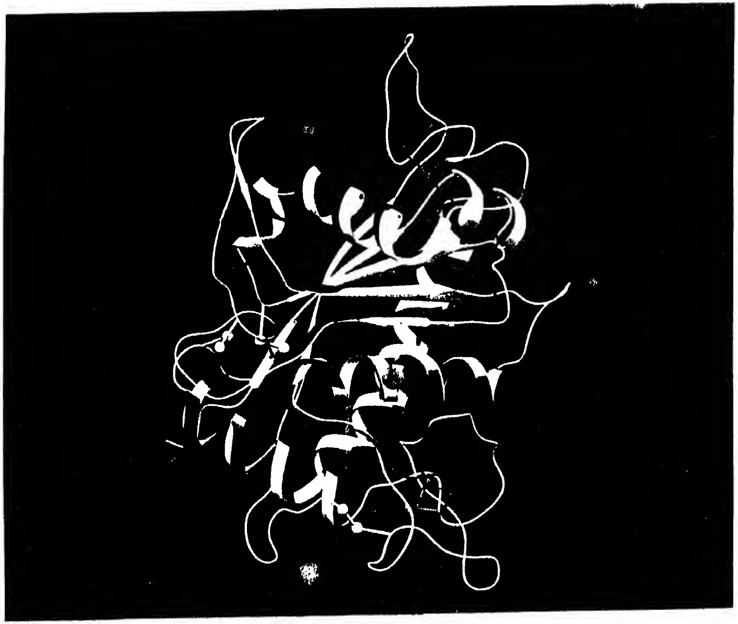
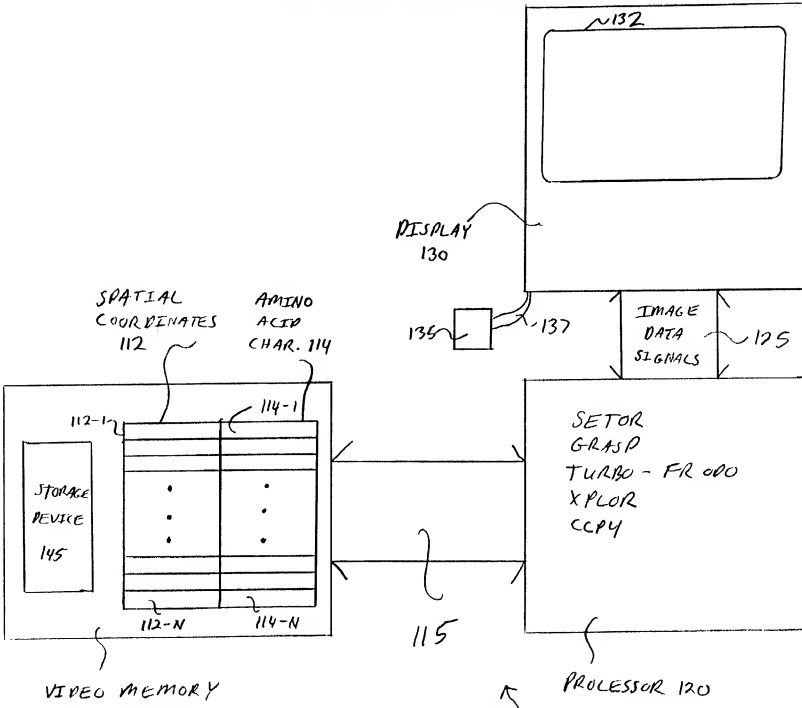


FIGURE 5



132
DISPLAY
130
135
137
IMAGE
DATA
SIGNALS
125
SPATIAL
COORDINATES
112
AMINO
ACID
CHAR. 114
114-1
112-1
STORAGE
DEVICE
145
112-N
114-N
115
SETOR
GRASP
TURBO - FRODO
XPLOR
CCP4
VIDEO MEMORY
110
PROCESSOR 120
1000

Fig. 6